

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 31, 2001, 16:29:53 ; Search time 31.09 Seconds

(without alignments)
3187.406 Million cell updates/sec

Title: US-09-250-083a-2

Perfect score: 3942
Sequence: 1 MSFIDPYQHIVHEQYSHKF.....LSNVEARRFNKEFLSKPKKA 749

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3738.5	94.8	748	6	Q9T38 oryctolagus
2	2964	75.2	563	4	Q9U16 homo sapien
3	732	18.6	1012	4	Q9U16 homo sapien
4	732	18.6	1012	4	Q9U16 homo sapien
5	499.5	12.7	541	4	Q9U16 homo sapien
6	494.5	12.5	541	4	Q9U16 homo sapien
7	259	6.6	637	3	Q9P82 cryptococu
8	256.5	6.5	634	3	Q9P81 filobasidie
9	228.5	5.8	626	3	Q42790 neurospora
10	225.5	5.7	626	3	Q42791 neurospora
11	223	5.7	608	3	Q93795 candida alb
12	216.5	5.5	640	3	Q59863 kluyveromyc
13	209.5	5.3	754	3	Q94046 candida alb
14	209.5	5.3	754	3	Q94046 candida alb
15	207.5	5.3	605	3	Q74207 candida alb
16	207.5	5.3	605	3	Q9UW6 candida alb
17	199	5.0	49	4	Q14064 homo sapien
18	194.5	4.9	633	3	Q9Y786 schizosacch
19	192.5	4.9	624	3	Q13857 schizosacch

20	178.5	4.5	574	10	Q9FY55 arabidopsis
21	172.5	4.4	510	10	Q9LX1 arabidopsis
22	171.5	4.4	493	10	P92940 arabidopsis
23	170.5	4.3	613	3	P78854 schizosacch
24	169	4.3	644	3	Q9UW5 schizosacch
25	163.5	4.1	673	3	Q9P327 schizosacch
26	153	3.9	528	10	Q9ZVY8 arabidopsis
27	144	3.7	583	10	Q9FYD9 arabidopsis
28	140.5	3.6	972	10	Q9M2D4 arabidopsis
29	140.5	3.6	2178	2	Q46149 clostridium
30	138.5	3.5	773	10	Q9M2R0 arabidopsis
31	135.5	3.4	505	10	Q48645 arabidopsis
32	129	3.3	1278	8	Q36586 lycopersico
33	128	3.2	1096	11	Q62688 rattus norv
34	126.5	3.2	2104	3	Q42730 schizosacch
35	126.5	3.2	2104	3	Q14157 schizosacch
36	126	3.2	694	4	Q9Y2J0 homo sapien
37	125	3.2	2874	14	Q9ODE2 cyphonectr
38	124.5	3.2	2048	4	Q9HBU3 homo sapien
39	124.5	3.2	2061	4	Q9NZM1 cyphonectr
40	124	3.1	2874	14	Q9ODE1 cyphonectr
41	122.5	3.1	1178	3	Q12527 cyphonectr
42	122	3.1	987	5	Q9V718 drosophila
43	121.5	3.1	769	10	Q9LXU2 arabidopsis
44	121	3.1	675	10	Q65279 arabidopsis
45	119	3.0	857	10	Q9Y0C8 arabidopsis

ALIGNMENTS

RESULT 1
Q9T38 PRELIMINARY; PRT: 748 AA.
ID Q9T38;
AC Q9T38;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PHOSPHATIDYL CHOLINE 2-ACYLHYDROLASE CPLA2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=HEART;
RA Al-Khalili O.K., Eaton D.C.;
RT Molecular cloning of cDNA coding for phospholipase A2.*;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF204923; AAF15299.1; -
DR HSSP; P47712; IBCI.
DR InterPro: IPR000008; -
DR InterPro: IPR000209; -
DR InterPro: IPR001596; -
DR InterPro: IPR002642; -
DR Pfam; PF00168; C2; 1.
DR Pfam; PF01735; PLA2_B; 1.
DR PROSITE; PS5004; C2 DOMAIN 2; 1.
DR PROSITE; PS00387; PPA2; UNKNOWN_1.
DR PROSITE; PS00136; SUBSTITLASE_ASP; UNKNOWN_1.
DR SMART; SM00239; C2; 1.
KW Hydrolase.
SQ SEQUENCE 748 AA; 85234 MW; 7661A3EFC41FF668 CRC64;

Query Match 94.8%; Score 3738.5; DB 6; Length 748;

Best Local Similarity 94.3%; Pred. No. 1.3e-279;
Matches 706; Conservative 26; Mismatches 16; Indels 1; Gaps 1;

QY 1 MSFIDPYQHIVHEQYSHKFVVVLRATKTKGAFGMDLPDPYVELFISTPDSRRRT 60
Db 1 MSFIDPYQHIVHEQYSHKFVVVLRATKTKGAFGMDLPDPYVELFISTPDSRRRT 60

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QY 61 RHFNNDINPNNETFEFLIDPNOENVLEITLMDANYMDETIGATFTVSSMKVGEKKEV 120
DB 61 RHFNNDINPNNETFEFLIDPNOENVLEITLMDANYMDETIGATFTVSSMKVGEKKEV 120
QY 121 PFIPOVNTVMVLEMSLEVSCDPLRFSMALCDEKTFROQRKREHIESKLLGPPNSGC 180
DB 121 PFIPOVNTVMVLEMSLEVSCDPLRFSMALCDEKTFROQRKREHIESKLLGPPNSGC 180
QY 181 LHSARDVPVVALISGGGFRAMVFGSVKALKYESGILDCATYVAGLSGSTMVSLYSH 240
DB 181 LKSTRVPVVALISGGGFRAMVFGSVKALKYESGILDCATYVAGLSGSTMVSLYSH 240
QY 241 PDPEPEKPEINEELMKVNSHNPDLTLPQYKRYVESLMKKSSGQVPTFDIFGMLIG 300
DB 241 PDPEPEKPEINEELMKVNSHNPDLTLPQYKRYVESLMKKSSGQVPTFDIFGMLIG 300
QY 301 EFLIHRMHTTSLSLKEKVSACPLPFTCLHVKPDVSELMAFADWVEFSPEIGMAKYG 360
DB 301 EFLIHRMHTTSLSLKEKVSACPLPFTCLHVKPDVSELMAFADWVEFSPEIGMAKYG 360
QY 361 TMAPDLESGKFFMGTVYKKEENPLHFLMGVGSASFILFRVLGVSOSRSGTMEEE 420
DB 361 TMAPDLESGKFFMGTVYKKEENPLHFLMGVGSASFILFRVLGVSOSRSGTMEEE 420
QY 421 LENTTKHIVSDSDSDSHPKGTENEDAGSDYQSDNOASWIRHIMALVSDSALFN 480
DB 421 LENTTKHIVSDSDSDSHPKGTENEDAGSDYQSDNOASWIRHIMALVSDSALFN 480
QY 481 TREGGKXHNMLGINTSYPLSPDPAFODSFDDDELAAVADPEFERIYEPDLV 540
DB 481 TREGGKXHNMLGINTSYPLSPDPAFODSFDDDELAAVADPEFERIYEPDLV 540
QY 541 KSKKIHVVDGTLFNLPLRPGQVDLIISFDSARPSDSSPEFKLLAEKAKANN 600
DB 540 KSKKIHVVDGTLFNLPLRPGQVDLIISFDSARPSDSSPEFKLLAEKAKANN 600
QY 601 KLPPEKIDYVDRGLKCYVFKPNPMDEKDCPTIHFVLANINFRKYKAPGVRETJ 660
DB 601 KLPPEKIDYVDRGLKCYVFKPNPMDEKDCPTIHFVLANINFRKYKAPGVRETJ 660
QY 660 EKEKIDPFIPODPSPEFTFNQYPNQAFKRLHDLMHFNLTNNIDVIEKAVESIEYRR 720
DB 660 EKEKIDPFIPODPSPEFTFNQYPNQAFKRLHDLMHFNLTNNIDVIEKAVESIEYRR 720
QY 721 QNPSRCSVLSNVEARFENKEFLSKPRA 749
DB 721 QNPSRCSVLSNVEARFENKEFLSKPRA 749
QY 720 QNPSRCSVLSNVEARFENKEFLSKPRA 748
DB 720 QNPSRCSVLSNVEARFENKEFLSKPRA 748

RESULT 2
Q0UIY6
AC 09UIY6 PRELIMINARY: PRT: 563 AA.
ID 09UIY6
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE DJ661G12.1 (TREMBLrel. 16, Last annotation update)
DE DJ661G12.1 (PHOSPHOLIPASE A2, GROUP IVA (CYTOSOLIC, CALCITUM-DEPENDENT)
DE (CP1A2-ALPHA)) (FRAGMENT).
GN PLA2G4A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Frankland J.;
RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL049797; CAB56229.1; -
DR InterPro; IPR000209; -
DR InterPro; IPR001596; -
DR InterPro; IPR002642; -
DR Pfam; PF01735; PLA2_B_1;
DR ProSite; PS00387; PPASE; UNKNOWN_1.

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DR PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
DR SMART; SM00022; PLAC; 1.
FR NON_TER
SQ SEQUENCE 563 AA: 63712 MW: DBA3A12D9D467C94 CRC64:

Query Match
Best Local Similarity 75.2%; Score 2964; DB 4; Length 563;
Matches 562; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Pred. NO. 4,4e-220;

QY 187 VPVVALISGGGFRAMVFGSVKALKYESGILDCATYVAGLSGSTMVSLYSH 246
DB 1 VPVVALISGGGFRAMVFGSVKALKYESGILDCATYVAGLSGSTMVSLYSH 246
QY 247 GPEEINEELMKVNSHNPDLTLPQYKRYVESLMKKSSGQVPTFDIFGMLIGTFLHN 306
DB 247 GPEEINEELMKVNSHNPDLTLPQYKRYVESLMKKSSGQVPTFDIFGMLIGTFLHN 306
QY 307 RMTTSLSLKEKVSACPLPFTCLHVKPDVSELMAFADWVEFSPEIGMAKYGTFMAD 366
DB 307 RMTTSLSLKEKVSACPLPFTCLHVKPDVSELMAFADWVEFSPEIGMAKYGTFMAD 366
QY 367 LFGSKFFMGTVYKKEENPLHFLMGVGSASFILFRVLGVSOSRSGTMEEELENTT 426
DB 367 LFGSKFFMGTVYKKEENPLHFLMGVGSASFILFRVLGVSOSRSGTMEEELENTT 426
QY 427 KHIIVSDSDSDSHPKGTENEDAGSDYQSDNOASWIRHIMALVSDSALFN 486
DB 427 KHIIVSDSDSDSHPKGTENEDAGSDYQSDNOASWIRHIMALVSDSALFN 486
QY 487 GKVHNMGLINTSYPLSPDPAFODSFDDDELAAVADPEFERIYEPDLVSKKIH 546
DB 487 GKVHNMGLINTSYPLSPDPAFODSFDDDELAAVADPEFERIYEPDLVSKKIH 546
QY 547 VVDGTLFNLPLRPGQVDLIISFDSARPSDSSPEFKLLAEKAKANN 606
DB 547 VVDGTLFNLPLRPGQVDLIISFDSARPSDSSPEFKLLAEKAKANN 606
QY 607 IDPYVDRGLKCYVFKPNPMDEKDCPTIHFVLANINFRKYKAPGVRETJ 666
DB 607 IDPYVDRGLKCYVFKPNPMDEKDCPTIHFVLANINFRKYKAPGVRETJ 666
QY 667 DEDIDDPSPSTFNQYPNQAFKRLHDLMHFNLTNNIDVIEKAVESIEYRONPSRC 726
DB 667 DEDIDDPSPSTFNQYPNQAFKRLHDLMHFNLTNNIDVIEKAVESIEYRONPSRC 726
QY 727 SVLSNVEARFENKEFLSKPRA 749
DB 727 SVLSNVEARFENKEFLSKPRA 749
QY 541 SVLSNVEARFENKEFLSKPRA 563
DB 541 SVLSNVEARFENKEFLSKPRA 563

RESULT 3
Q05712
AC 095712 PRELIMINARY: PRT: 1012 AA.
ID 095712
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE DJ661G12.1 (TREMBLrel. 16, Last annotation update)
DE DJ661G12.1 (PHOSPHOLIPASE A2 BETA.
DE CYTOSOLIC PHOSPHOLIPASE A2 BETA.
GN CPA2 BETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-99185108; PubMed-10085124;
RA Pickard R.T., Striffler B.A., Kramer R.M., Sharp J.D.;
RT "Molecular cloning of two new human paralogs of 85-kDa cytosolic
RL phospholipase A2."
DR EMBL; AF065215; AAC78836.1; -
DR InterPro; IPR000008; -

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Db      842 ICLLVGYLINSCLPLQPTRDVDLISLDYNLGA-----FOOQLGRCOEQGIGF 896
Oy      605 PRIDPVFREGKCYVYK-PKNPDMKDCPTIHFVLANINRYKAGVPRETEEEK 663
Db      897 PRISPEEQLOPRECHTSPTPC-----GAPAVLHFLYVSOFREYSAPGV-RRTPEEA 951
Oy      664 EIADFDIDDPESPSTFNFOYPNQAFKRLHDLMHENTLNINDIVKEAVESIEYRQ 721
Db      952 AAGEVNL-SSSDSPYHYTKVTVYSGEDVDKLLHLTHYVNCNNGQLLEALRQAVRRQ 1008

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RESULT 5

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ID      075457      PRELIMINARY;      PRT;      541 AA.
AC      075457;
DT      01-NOV-1998 (TREMBLrel. 08, Created)
DT      01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT      01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE      CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX      NCBI_TaxID=9606;
RN      (1)
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98371032; PubMed=9705332;
RA      Underwood K.W., Song C., Kriz R.W., Chang X.J., Knopf J.L., Lin L.L.;
RT      "A novel calcium-independent phospholipase A2, cPLA2 gamma, that is
RT      preylated and contains homology to cPLA2."
RL      J. Biol. Chem. 273:21926-21932(1998).
DR      EMBL; AF058921; AAC32823.1; -
DR      InterPro: IPR002642; -
DR      Pfam: PF01735; PLA2_B; 1.
DR      SMART; SM00022; PLAC; 1.
SQ      SEQUENCE 541 AA; 60920 MW; BBB972A611FB5237 CRC64;

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Query Match 12.7%; Score 499.5; DB 4; Length 541;
 Best Local Similarity 27.0%; Pred. No. 4.5e-30;
 Matches 150; Conservative 88; Mismatches 189; Indels 129; Gaps 20;

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Oy      135 SLEVSCPDRLFSMALCDEKTFROQRKEHIRESMKKLGPKNSEGLSARDVPVAALG 194
Db      3 SEEVSIIPQLQ-----KEKAVERRRRLHVLKALKL-----RIADAPVAVAVG 48
Oy      195 SGGGRAMVGFSGVYKALYESGILDCATYVAGISGTWMTLYSHPDPEKPEEINEE 254
Db      49 SGGGLRAHIAACGLVLESEMKEGILDAVYLAGVSGSTWAISSLYTN-----DGDMEALEA 103
Oy      255 LKKNVSHNPLLLTPQKVRVYESLMKKKSGQPV-----FTTDFGMILGETLIH 305
Db      104 DLKH-----RFTROEMDLAKSLQKTIQAARSENYSLTDWMAVMVSKOTR 148
Oy      306 NRMNTTSLSEKRVNTAOCPLPLFTCL--HKRPVSELMFAD-WVEFSPEYETGMAYGTF 362
Db      149 ELPESHLSNMKKRPVEEGTLPRPIFAIDNDLOPSMOEARAPETWEFTPHHAGFALGAF 208
Oy      363 MAPDLFGSFEPFGVYKKKEENPLHFLMGVMSAPSIENRVLVSGSGSRST----- 416
Db      209 VITTHGSKFKKGRVLRHPRDLTFRLGLWGSAL-----GNTVEYIREY 252
Oy      417 MEELLENITTKHI-----VSNDSS-----DSDESHEPKGTENEDAGSDYOD 459
Db      253 IFDQLRNLTGLKLMRAVANAKSIGHLIFARLLRQESSOGGHPPP-----EDBG-----GE 304
Oy      460 NOASWIHRI-----MALVSDSALFNTREGRAKGVNFMGLNLTSTYPLSPSPATOD 514
Db      305 PEHTWLTLEMWTRTSLEKQOPHEDPE-RKGSLSNLM-----DEVKKT 348
Oy      515 SPDDDELDAVAADPDEFE--IYEPIDVYSKKIHVVDSTLTNLPPLRQPGVDLI 572

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Db      349 GICASKWEGTTHNPLYKHGIRDKIMSRKHLHLVDAGLAINTPPVLPPTREVHLIL 408
Oy      573 SFDESARPSDPPPEKELLAEKMAKMKLPPPKIDPYFD--REGKCYVYKFKKPNPM 630
Db      409 SFDFSA-----GDPEFTIATDYCRHKRIFFQVDEALDLSKAPACIYLKGETG-- 461
Oy      631 EKDCPTIHFVLANIN 646
Db      462 ----PVYIHFPLEFND 473

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RESULT 6

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ID      09UP65      PRELIMINARY;      PRT;      541 AA.
AC      09UP65;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE      CYTOSOLIC PHOSPHOLIPASE A2 GAMMA.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX      NCBI_TaxID=9606;
RN      (1)
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99185108; PubMed=10085124;
RA      Pickard R.T., Striffler B.A., Kramer R.M., Sharp J.D.;
RT      "Molecular cloning of two new human paralogs of 85-kDa cytosolic
RT      phospholipase A2."
RL      J. Biol. Chem. 274:8823-8831(1999).
DR      EMBL; AF065214; AAC78835.1; -
DR      InterPro: IPR002642; -
DR      Pfam: PF01735; PLA2_B; 1.
DR      SMART; SM00022; PLAC; 1.
SQ      SEQUENCE 541 AA; 60948 MW; 63E6AE7E7550741 CRC64;

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Query Match 12.5%; Score 494.5; DB 4; Length 541;
 Best Local Similarity 26.8%; Pred. No. 1.1e-29;
 Matches 149; Conservative 88; Mismatches 190; Indels 129; Gaps 20;

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Oy      135 SLEVSCPDRLFSMALCDEKTFROQRKEHIRESMKKLGPKNSEGLSARDVPVAALG 194
Db      3 SEEVSIIPQLQ-----KEKAVERRRRLHVLKALKL-----RIADAPVAVAVG 48
Oy      195 SGGGRAMVGFSGVYKALYESGILDCATYVAGISGTWMTLYSHPDPEKPEEINEE 254
Db      49 SGGGLRAHIAACGLVLESEMKEGILDAVYLAGVSGSTWAISSLYTN-----DGDMEALEA 103
Oy      255 LKKNVSHNPLLLTPQKVRVYESLMKKKSGQPV-----FTTDFGMILGETLIH 305
Db      104 DLKH-----RFTROEMDLAKSLQKTIQAARSENYSLTDWMAVMVSKOTR 148
Oy      306 NRMNTTSLSEKRVNTAOCPLPLFTCL--HKRPVSELMFAD-WVEFSPEYETGMAYGTF 362
Db      149 ELPESHLSNMKKRPVEEGTLPRPIFAIDNDLOPSMOEARAPETWEFTPHHAGFALGAF 208
Oy      363 MAPDLFGSFEPFGVYKKKEENPLHFLMGVMSAPSIENRVLVSGSGSRST----- 416
Db      209 VITTHGSKFKKGRVLRHPRDLTFRLGLWGSAL-----GNTVEYIREY 252
Oy      417 MEELLENITTKHI-----VSNDSS-----DSDESHEPKGTENEDAGSDYOD 459
Db      253 IFDQLRNLTGLKLMRAVANAKSIGHLIFARLLRQESSOGGHPPP-----EDBG-----GE 304
Oy      460 NOASWIHRI-----MALVSDSALFNTREGRAKGVNFMGLNLTSTYPLSPSPATOD 514
Db      305 PEHTWLTLEMWTRTSLEKQOPHEDPE-RKGSLSNLM-----DEVKKT 348
Oy      515 SPDDDELDAVAADPDEFE--IYEPIDVYSKKIHVVDSTLTNLPPLRQPGVDLI 572
Db      349 GICASKWEGTTHNPLYKHGIRDKIMSRKHLHLVDAGLAINTPPVLPPTREVHLIL 408

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OY 573 SFDPSARPSDSSPPFKELLAEKMAKNKLPPFKIDPYED--REGLECYVFKPNPDM 630
DB 409 SFDPSA-----GDPFETIRATDYCRHRKIPFOVEAEELDMSKAPASCIYLLKGEIG-- 461
OY 631 EKDCPTIIFHVLANIN 646
DB 462 ----PVMMHFFLEPNID 473

RESULT 7
OY 098P2 PRELIMINARY: PRT: 637 AA.
AC 098P2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE SECRETED PHOSPHOLIPASE B.
GN PLB1.
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_Taxid=5207;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H99;
RA Cox G.M., McNamee H.C., Gottfredsson M., Chen S.C.A., Wright L.C.,
RT Sorrell T.C., Ghanoun M.A., Perfect J.R.;
RL "Phospholipase B is a virulence factor for Cryptococcus neoformans.";
EMBL: AF223383; AAF65220.1; -
DR InterPro: IPR002642; -
DR Pfam: PF01735; PLA2_B.1.
DR SMART: SM00022; PLAC.1.
SO SEQUENCE 637 AA; 68789 MW; C37B9799D69A9330 CRC64;

Query Match 6.6%; Score 259; DB 3; Length 637;
Best Local Similarity 24.1%; Pred. No. 2.1e-11;
Matches 111; Conservative 67; Mismatches 145; Indels 138; Gaps 20;

OY 154 EKFFROQRKHIESKMKLLGPKNSBGLHSARDVPVVAIIIGSGGFFRAMV-GFSGVYKAL 212
DB 65 ERAVTEAREKLVQPAIEQMA--ARGLTPPPTPTNGVALSGGYRAMLTGLGIGMM 121
OY 213 YES-----GILDCATVAGISGSTMWSTLYSHPDPEKPEEINELMKVSHNP 263
DB 122 NESTEASESETGMDGVSTWAGISGSGWATGTFMSNG--QLPTNLENLW-NIDSN- 176
OY 264 LLLTPQKVRVYESLWK---KKSSGQPVTFDIFGMLIGETL-----IHNRMNTLSS 314
DB 177 LVPPDDDKLSFYETETNAKSDGLGPIQITDYMGLAISHVLPERYQJNSTNPULTFSS 236
OY 315 LKRVN---TAQCPPLPFTCLHVK-PDVSELMAD---WVESPYEIGMAKYG-T-FMAP 365
DB 237 LPVSVALGNASLPMPIIADRRKREAGELVIAENATVW-EFTPYEFGSWAGSQYKSP 295
OY 366 DLGSKFPMGTVYKKEEN-----PLHFLMGVWGSASFILFNRLVGVSGSGSRSTM 417
DB 296 GAFTPEIYLGTSYDGSPTGCKGFDQLSFVWGTSAITLNGAF---LELNGTDS----- 347
OY 418 EEELENTTKHIVSNDSDSDSHKPTENEDAGSDYOQSDNOASWIMHIMIALVSDSA 477
DB 348 -GLLTNLITA-FLADLGEQDADISRIPTFSNNSGE----- 382
OY 478 LFNTREGRAKGVNFMGLNLTSTPLSPDPAFODSFDDDELDAVADPDEFERIYEP 537
DB 383 -----NPIYNLT----- 389
OY 538 LDVYSKRIHVVDGLT-FNLPPPLIRPORGVDLISFDS 577
DB 390 -----YTLVDAGETNPIPLEPLVPTRODVAIVAFDSS 424
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RESULT 8
OY 098P1 PRELIMINARY: PRT: 634 AA.
AC 098P1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE PHOSPHOLIPASE B.
GN PLB.
OS Filobasidiella neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_Taxid=40410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B-3501;
RA Varma A., Kwon-Chung K.J.;
RT "The phospholipase B gene from a serotype D isolate of Cryptococcus
neoformans.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AF238241; AAF61964.1; -
DR InterPro: IPR000874; -
DR InterPro: IPR002642; -
DR Pfam: PF01735; PLA2_B.1.
DR PROSITE: PS00257; BOMBESIN; UNKNOWN_1.
DR SMART: SM00022; PLAC.1.
SO SEQUENCE 634 AA; 68167 MW; E2998B83CFADA925 CRC64;

Query Match 6.5%; Score 256.5; DB 3; Length 634;
Best Local Similarity 23.2%; Pred. No. 3.2e-11;
Matches 107; Conservative 73; Mismatches 139; Indels 143; Gaps 19;

OY 154 EKFFROQRKHIESKMKLLGPKNSBGLHSARDVPVVAIIIGSGGFFRAMV-GFSGVYKAL 212
DB 65 ERAVTEAREKLVQPAIEQMA--ARGLTPPPTPTNGVALSGGYRAMLTGLGIGMM 121
OY 213 YES-----GILDCATVAGISGSTMWSTLYSHPDPEKPEEINELMKVSHNP 263
DB 122 NESTEASESETGMDGVSTWAGISGSGWATGTFMSNG-----QLPTNLENLW-NID 174
OY 264 LLLTPQKVRVYESLWK---KKSSGQPVTFDIFGMLIGETL-----IHNRMNTL 312
DB 175 SNLVFPDDGLSFYNTETNAKSDGLGPIQITDYMGLAISHVLPERYQJNSTNPULTF 234
OY 313 SSKKRY---NTAQCPLPFTCLHVKPDVSELMAD---WVESPYEIGMAKYG-T-FMA 364
DB 235 SSLPSVVALGNASLPMPIIIVV--AERREAGELVIAENATVW-EFTPYEFGSWAGSQYKS 291
OY 365 PDLGSKFPMGTVYKKEEN-----PLHFLMGVWGSASFILFNRLVGVSGSGSRSTM 416
DB 292 PGAFTEIYLGTSYDGSPTGCKGFDQLSFVWGTSAITLNGAF---LELNGTDS----- 344
OY 417 EEELENTTKHIVSNDSDSDSHKPTENEDAGSDYOQSDNOASWIMHIMIALVSDS 476
DB 345 -GLLTNLITA-FLADLGEQDADISRIPTFSNNSGE----- 379
OY 477 ALFNTREGRAKGVNFMGLNLTSTPLSPDPAFODSFDDDELDAVADPDEFERIYEP 536
DB 380 -----NPIYNLT----- 386
OY 537 LDVYSKRIHVVDGLT-FNLPPPLIRPORGVDLISFDS 577
DB 387 -----YTLVDAGETNPIPLEPLVPTRODVAIVAFDSS 421
```

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RESULT 9
OY 042790 PRELIMINARY: PRT: 626 AA.
AC 042790;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, last sequence update)
```

DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE LYOPHOSPHOLIPASE.
 GN LPL.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ST. LAWRENCE ST7A-OR3-IVA;
 RA Catchside D.E.A., Yeaton P.J.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF045574; AAC03052.1; -
 DR InterPro; IPR002642; -
 DR Pfam; PF01735; PLA2_B; 1.
 DR SMART; SM00022; PLAC; 1.
 DR SMART; SM00022; PLAC; 1.
 SQ SEQUENCE 626 AA; 67586 MW; 2158D0EDA26E0CDB CRC64;

Query Match 5.8%; Score 228.5; DB 3; Length 626;
 Best Local Similarity 23.7%; Pred. No. 4.5e-09;
 Matches 117; Conservative 62; Mismatches 155; Indels 159; Gaps 20;

QY 142 PDRESMALCDEKTFROQKREHRESMKLLGPKN-----SEGLHSARDVPVYA 191
 DB 36 PTLRKAVDLSNEKKNMLSTRKNTIOPMRDLKRAITGFDETFEPMNANNISQLPNVA 95
 QY 192 ILGSGGFRAMGFGSVMAIYE-----SGILDCAITYVAGLSGTWYMTLSYSH 240
 DB 96 IAISSGGYRALMGAGFVAADNRIONTTGAGIGGLGSLSTYLAGLSGGWLVGSLFSN 155
 QY 241 P-----DFPE---KGPEINEELMKVSHNPILLTPQKRYVE---SLM 280
 DB 156 NFSSTFTLSEKKVDFENSIFKPREAG-----LSTVNRIOYSEVAKEVA 202
 QY 281 KKKSSQPYTFDIDGMLIGETLIHNRN---TTLSLKEKYN---TAOCPLPFTCLHVK 335
 DB 203 KKKDAFFETSIDYNGRALSYOLIGADMGCPAYTFESSIAOTNFOKAETPFIIVADGRA 262
 QY 336 P-DVSELMFADWVESPFIYGM---AKYGTAPAPDLFGSKFPMGYVK---KYE--NPLH 387
 DB 263 PGDTTISLNTATYERNPEFTGMDPTVYG-FAPTKYLGANFNGVYIPSGCKVEGLDQAG 321
 QY 388 FLMGWGAFAFSLIFNRVLGVSQSGSGSTMEEBLENTTKHIVSNDSDDESHEPKGT 447
 DB 322 FVMG-----TSSTLFNGFL-----LANISSYDVARAHHSRDFC--PQGN 360
 QY 448 -ENEDAGSDYQSDNQASWIRHIMALVSDSALFNTREGRAKGVHFMCLNLTSTPLSP 506
 DB 361 RROEDDVSQLIPNPLDMNRR-----381
 QY 507 LSDFATQDSFDDDELDAVAADPDEFERIEPLDYKSKTIHVVDGSLTF-NLPYPLILRPQ 565
 DB 382 -----TNPADLTLELD-----LVDGGEIDLONTPLNPLTPQV 412
 QY 566 RGVVDLIISDFESA 578
 DB 413 RAVDVIFAVDSSA 425

RESULT 10
 ID 042791 PRELIMINARY; PRT; 626 AA.
 AC 042791;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE LYOPHOSPHOLIPASE.
 GN LPL.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LINDEGREEN 25A.
 RA Catchside D.E.A., Yeaton P.J.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF045575; AAC03053.1; -
 DR InterPro; IPR002642; -
 DR Pfam; PF01735; PLA2_B; 1.
 DR SMART; SM00022; PLAC; 1.
 DR SMART; SM00022; PLAC; 1.
 SQ SEQUENCE 626 AA; 67527 MW; E11B3B059E4E8C2 CRC64;

Query Match 5.7%; Score 225.5; DB 3; Length 626;
 Best Local Similarity 23.8%; Pred. No. 7.6e-09;
 Matches 118; Conservative 63; Mismatches 151; Indels 163; Gaps 23;

QY 142 PDRESMALCDEKTFROQKREHRESMKLLGPKN-----SEGLHSARDVPVYA 191
 DB 36 PTLRKAVDLSNEKKNMLSTRKNTIOPMRDLKRAITGFDETFEPMNANNISQLPNVA 95
 QY 192 ILGSGGFRAMGFGSVMAIYE-----SGILDCAITYVAGLSGTWYMTLSYSH 240
 DB 96 IAISSGGYRALMGAGFVAADNRIONTTGAGIGGLGSLSTYLAGLSGGWLVGSLFSN 155
 QY 241 P-----DFPE---KGPEINEELMKVSHNPILLTPQKRYVE---SLM 280
 DB 156 NFSSTFTLSEKKVDFENSIFKPREAG-----LSTVNRIOYSEVAKEVA 202
 QY 281 KKKSSQPYTFDIDGMLIGETLIHNRN---TTLSLKEKYN---TAOCPLPFTCLHVK 335
 DB 203 KKKDAFFETSIDYNGRALSYOLIGADMGCPAYTFESSIAOTNFOKAETPFIIVADGRA 262
 QY 336 P-DVSELMFADWVESPFIYGM---AKYGTAPAPDLFGSKFPMGYVK---KYE--NPLH 387
 DB 263 PGDTTISLNTATYERNPEFTGMDPTVYG-FAPTKYLGANFNGVYIPSGCKVEGLDQAG 321
 QY 388 FLMGWGAFAFSLIFNRVLGVSQSGSGSTMEEBLENTTKHIVSNDSDDESHEPKGT 447
 DB 322 FVMG-----TSSTLFNGFL-----LANI-----339
 QY 448 ENEDAGSDYQSDNQASWIRHIMALVSDSALFNTREGRAKGVHFMCLNLTSTPLSP 507
 DB 340 -----SSY--DGVARRAR-----GR-----353
 QY 508 SDPATQ-DSFDDDELDAVAADP-DEFERIEPLDYKSKTIHVVDGSLTF-NLPYPLILRPQ 563
 DB 354 -DFPCQGNRROEDDVSQLIPNPLDMNRRTPNAD--TLELDVDBGEDLONTPLNPLTPQ 410
 QY 564 RGVVDLIISDFESA 578
 DB 411 PVRAVDVIFAVDSSA 425

RESULT 11
 ID 093795 PRELIMINARY; PRT; 608 AA.
 AC 093795;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE PHOSPHOLIPASE B.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sugiyama Y., Nakashima S., Nozawa Y., Kitaajima Y., Mirbod F.;
 RT "Molecular cloning of phospholipase B 2 from Candida albicans.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB010809; BAA36162.1; -
 DR InterPro; IPR002642; -
 DR Pfam; PF01735; PLA2_B; 1.

DR SMART, SM00022, PLAC, 1.
SQ SEQUENCE 608 AA; 67219 MW; 0ABEA2C878CD8610 CRC64;

Query Match 5.7%: Score 223; DB 3; Length 608;
Best Local Similarity 23.1%: Pred. No. 1.1e-08;

Matches 95; Conservative 68; Mismatches 164; Indels 84; Gaps 15;

QY 141 CPDLRSMALCD-----OETFRQORKEHIESMKLLGPKRNSGLHSARDY-----187
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 31 CPBGLKLRSLDGINSEKAYIDRYANAKSELRF-----LHNAKAVDFVDGFLN 82
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 188 -PVALILSGGGRFANVGSVKALYE-----SGILDATYVAGISGTSWSTL 237
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 83 SNPLIGLAFGGGGRFAMLAGAGELLADSRATNPVSGLIÖSSSYIVGLSGGSMVLSL 142
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 238 YSHDPPEKPEEINELMKVNSHNPILLTPQVKRYVESLW-----KKSSGQPV 289
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 143 ASDNLLPV--DÖLREKLMWDI--ONSLVAYYGVNIVRNT--AMGNINILQYOTKOLAGFTV 198
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 290 TTFDIFGLIGETLIHNRMTTSLKEKYNTA-----OCPLPLFTCLHVKPVSELMF 343
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 199 SIIDVYRALSHQULTTFDÖGASFMSDVTETTSFQNNEMPRPIIALGREFPTVLNMF 258
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 344 ADWV-EFSPEYIGN--AKYGTMAPDLFGSKFPMGVYKRYEENPLH--FLMGVWSAF 397
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 259 NSYFELTFPEVGSMDPSLSFVDYTKYIGTRLDGAPVSKCVNGFNDAGFFMGTSSS-- 316
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 398 SILFNRLVYSGSGSRGSTRMEELNTTKHIVS-----NDSSDSDESHEP 444
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 317 --LENYLQQLNNPIPPFKELISKFTLDEVEKLNIDIAQYNPNPHKSNNSDTKIAQS 374
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 445 KGTENAGSDYQSDNOASWIRHIMALVS-----DSALFNTR 483
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 375 RLYLADGCGEDGQVPLPLIHRKVAIFAEDQADKNNMPDGSALIKTFE 425
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 12
059863 ID 059863 PRELIMINARY; PRT; 640 AA.

AC 059863;
DT 01-AUG-1998 (TEMBLrel. 07, Created)
DT 01-AUG-1998 (TEMBLrel. 07, last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, last annotation update)
DE PHOSPHOLIPASE B.
GN KLPB.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 1090;
RA Oishi H., Morimoto T., Watanabe Y., Tamai Y.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB014495; BAA28619.1;
DR InterPro: IPR002642;
DR Pfam: PF01735; Pfam2.B: 1.
DR SMART; SM00022; PLAC; 1.
SQ SEQUENCE 640 AA; 69982 MW; 90A696CB5D7FF9E3 CRC64;

Query Match 5.5%: Score 216.5; DB 3; Length 640;
Best Local Similarity 20.2%: Pred. No. 3.9e-08;

Matches 134; Conservative 100; Mismatches 233; Indels 195; Gaps 28;

QY 138 VCSGPD---LRFSMALCDEKTFRQORKEHIESMKLL-----GPKNS---EGLSHA 184
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 36 VVDCDENINLYRKADAVSDDEADWLKVRHSTVPALDKQFGKFTNDISIDKLILAT 95
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 185 RD-VPVVAILLGGGGRFANVGSVKALYE-----SGILDATYVAGISGTSWY 233
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 96 QDAPKVAIALCSGGGRFAMLAGAGELLADSRATNPVSGLIÖSSSYIVGLSGGSMVLSL 155
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 234 MSTL-YSHDPPEKPEEINEEL-----MKVNSHNPILLTPQVKRY--VESIMKKSS 285
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 156 VGLTAYNNMTSVQAIINNMTDONSIMDISNSIVPGISINIFSSISRWDDISDAVEEKKA 215
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 286 GQPTFTDIDIGMLIG-----ELLHNRMTTSLSK--EKVNTACPLPLTCLHVKRDVS 339
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 216 GFNTSIDVWGRALSYNFFPSLDGGVGYTWNLTRDQVFRKNGEMPPPIISAAGRYPGTQ 275
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 340 EL-MFADWVEFSPEYIGMAYKGFMAPDLFGSKFPMGVYKRYEENPLHFLMGVWSAFS 398
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 276 VVINATVFEENPEPKSMDY-----TLHFTDV-----304
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 399 ILFNRLVYSGSGSRGSTRMEELNTTKHIVNSDSDSDSHPRGTENEDAGSDYQS 458
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 305 -----RYAGTNVNGFTPNVTKCVAGFDNTG-----330
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 459 DNOASWIRHIMALVSALFNTRGRAGKVNHMLGLNLN--TSYPLSLSPATQDSF 516
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 331 -----FVNGTSSSLFN-----OPLQLNTDTLPSFLYNLHGLFTDASD 369
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 517 DDDELAAVADPDEFERIEPLDYKSK-----KIHVDSGLT-FNLPLYLILRPR 566
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 370 DYDDISIMAPNP-----FTEITNIPSNYSOSISEDDTLIVDGGEDCONPLPLQTER 424
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 567 GVDLILSFDESARPSDSSPPFKELLAEKNAKM-----NKLPFKI-DPYVFDREGLEK 620
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 425 EIDVIFALDNSADTDQSWP--DGSFLQTYARQGLQKGKIAFYVYDVNFTMLGLNTR 482
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 621 YVF--KPKN-PDMKDCPTIHFVLNINFRKYAKGVPRETEEKELADFIDDPES 676
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 483 PTFPGCDARNLTDESIPPLVYVMPNTRSEF-----NS 515
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 677 PESTFENQY-PNOAFKRLHLMHFNLTNID-----VTKEMAVSEIEYRQNP 724
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 516 NTFKMSYSTSEKFKMIQNGFEAVYMNKLTNDENFGCISCALRRKÖESLNTTL--PS 573
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 725 RC 726
DB 574 EC 575

RESULT 13
094046 ID 094046 PRELIMINARY; PRT; 754 AA.

AC 094046;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, last annotation update)
DE LYSOPHOSPHOLIPASE.
GN CA1C10.12.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1161;
RA Taylor K., Harris D.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1161;
RA Barrett B.G., Rajandream M.A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=1161;
RX MEDLINE=97435544; PubMed=9290243;
RA Tait E., Simon M.C., King S., Brown A.J., Gow N.A.R., Shaw D.J.;
RT "A Candida albicans genome project: cosmid contigs, physical mapping, and gene isolation."
RL Fungal Genet. Biol. 21:308-314(1997).

DR EMBL, AL033501; CAA11996.1; -.
DR InterPro; IPR02642; -.
DR Pfam; PF01735; PLA2_B; 1.
DR SMART; SM00022; PLAC; 1.
SQ SEQUENCE 754 AA; 81412 MW; 8291D959B05B554 CRC64

Query Match	5.3%	Score 209.5	DB 3	Length 754
Best Local Similarity	20.0%	Pred. No. 1.8e-07		
Matches 129	Conservative 99	Mismatches 206	Indels 21	Gaps 30

[illegible]

RESULT	ID	PRELIMINARY;	PRT;	754 AA.
09UVX1	ID_09UVX1			
AC	Q9UVX1;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAY-2001 (TREMBLrel. 16, Last annotation update)			
DE	PUTATIVE PHOSPHOLIPASE B PRECURSOR.			
GN	PLBL1.			
OS	Candida albicans (Yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Mitosporic Saccharomycetales; Candida.			
OX	NCBI_TaxID=5476;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SS;			
CA	Theils S., Koehler G.A.;			

```

RT      "putative phospholipase B precursor of Candida albicans."
RL      Submitted (DDB011997) to the EMBL/Genbank/DBD databases.
DR      EMBL: AF0381328; AAC008980.1; -.
DR      InterPro: IPR001522; -.
DR      InterPro: IPR002642; -.
DR      Pfam: PF01735; PLA2_B; 1.
DR      ProDom: PD002221; -. 1.
DR      SMART: SM0022; PLAC; 1.
SQ      SEQUENCE 754 AA; 81414 MW;  EA45653D5227B752 CRC64;

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Query Match	5.3%;	Score 209.5;	DB 3;	Length 754;
Best Local Similarity	20.0%;	Pred. No. 1.8e-07;		
Matches 129;	Conservative 98;	Mismatches 207;	Indels 211;	Gaps 30;

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0Y 140 SCPP-----LRF$MALCDEKTFRQORKEHTR$SKLLJGPN$N$GL$H$AR-----DVP-- 188
Db 114 TQPSKRTTIR$ASELSQDEKDYIKRQRTTKNLLIDFL$KRANL$D$PD$AS$FIN$D$APNH 173
0Y 189 ---VVAII$GGG$FRAMWQF$GVMKAL--YE-----SGILDCATYVAI$G$STWY$M$ST 236
Db 174 NITLISF$SGG$GYRAMLAGAQIILGLDORYEDANKH$GIGL$LD$STYVWG$SG$MNL$Y$G$S 233
0Y 237 LY$H$D$F$E$K$E$K$E$P$E$E$L$N$E$---L$K$N$V$H$N$P$L$L$L$T$Q$K$Y$K$Y$---V$E$S$L$M$K$K$S$Q$P$V 289
Db 234 LALN-DML$V$G-DIYNGK$STI$M$Q$D$S$TILN$SG$R$IK$D$T$A$Y$Y$G$LA$Q$A$Q$E$D$A$G$F$Q$T 291
0Y 290 T$T$D$F$G$M$L$I$G$E$T$E$T$L$H$-----N$B$N$T$T$S$L$K$--E$K$V$N$T$A$O$C$P$L$F$T$C$L$H$V$P 336
Db 292 S$V$T$D$W$G$A$L$S$Y$Q$F$E$E$D$D$S$T$G$G$A$N$T$W$S$IR$L$S$F$Q$D$H$S$M$Y$P$LV$A$N$G$R$T$P$Y$II 351
0Y 337 D$V$E$L$M$P$A$D$W$E$F$S$P$E$Y$E$G$M$K$A$K$T$E$N$A$P$D$L$--F$G$S$F$E$M$Q$T$Y$V$K$K$E$E$N$P$L$H$----- 387
Db 352 N$E$N$S$T$IF-----EIS$Y$E$E$G$S-----M$D$P$S$L$K$S$F$D$IO$Y$E$G$S$V$N$G$N$P$N$T$D$C$V$N$M$D 401
0Y 388 ---F$M$G$V$G$S$A$F$S$IL$E$F$R$V$L$G$V$G$S$Q$S$R$G$T$M$E$E$L$E$N$T$T$K$R$I$V$S$N$D$S$D$S$D$E$S$H$P 444
Db 402 N$A$G$F$M$T$G$I$S$S$S$---L$E$N$Q$IL-----L$Q$D$N$T$S$IN$S$IT----- 430
0Y 445 K$G$T$E$N$E$D$A$G$S$D$Y$Q$S$D$Q$A$S$W$I$H$R$I$M$A$L$V$S$D$A$L$E$N$T$R$E$G$R$A$K$V$H$N$M$L$G$L$N$T$S$Y$P$ 504
Db 431 -----K$M$I$E$K$V----- 437
0Y 505 S$P$L$S$F$A$T$Q$D$S$F$D$D$E$L$D$A$A$V$A$D$D$E$F$E$R$I$E$P$L$D$V$S$---K$K$H$V$Y$D$S$G$L$F$-N$L$P$P 559
Db 438 -LTDV$S$-----B$E$E$D$IA$Y$E$N$P$E$F$G$-D$S$A$G$IS$T$T$N$D$T$L$Y$LC$D$G$E$D$Q$N$P$Y 488
0Y 560 LIL$R$Q$R$C$V$D$L$IL$S$F$S$A$R$P$D$S$S$P$E$K$E$L$--L$A$E$K$M$A$M$K$-L$P$P$K$ID$P$Y$--V$F$D$R 614
Db 489 P$L$I$Q$N$E$R$V$D$T$F$A$D$N$A$D$N$S$M$P$N$T$S$I$Q$E$Y$K$K$O$F$S$G$K$G$C$T$P$P$R$A$P$D$Y$K$T$F$L$D$K 548
0Y 615 E$G$L$E$C$Y$F$K$K$R$N$D$M$E$-----K$D$C$P$T$I$H$F$V$L$A$N$I$N$F$R$K$Y$A$P$G$V$P$R$E$T$E$E 661
Db 549 N$M$G$D$P$V$E$F$G$C$N$S$D$E$L$V$A$M$H$E$N$D$K$I$N$Y$D$V$L$Y$V$Y$T$S$N$T$R$M$S$Y$----- 594
0Y 662 E$K$E$L$A$D$P$D$I$P$D$D$E$S$P$S$T$E$F$N$Q$P$R$N$C$-A$F$R$A$D$L$H$M$F$N$T$L$N$N$I 705
Db 595 -----N$S$N$E$T$F$L$A$S$D$Q$K$E$G$A$I$N$G$E$T$Y$V$R$N$M$ 626

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RESULT	15	
074207		
ID	074207	PRELIMINARY;
AC	074207;	PRT; 605 AA.
DT	01-NOV-1998 (TIREMBLrel. 08, Created)	
DT	01-NOV-1998 (TIREMBLrel. 08, Last sequence update)	
DT	01-MAR-2001 (TIREMBLrel. 16, Last annotation update)	
DE	PHOSPHOLIPASE B.	
GN	PLB.	
OS	Candida albicans (Yeast).	
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes	
OC	Saccharomycetales; mitosporic Saccharomycetales; Candida.	
OX	NCBI_TaxID=5476;	

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 31, 2001, 16:30:13 ; Search time 12.84 Seconds

(without alignments)
1998.237 Million cell updates/sec

Title: US-09-250-083A-2

Sequence: 3942
1 MSFIDPYOHIVHQSHEK.....LSNVEARRFENKEFLSKPKA 749

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3942	100.0	749	PA2Y_HUMAN	P47712 homo sapien
2	3793	96.2	749	PA2Y_HORSE	O77793 equus caball
3	3752	95.2	752	PA2Y_RAT	P50393 rattus norv
4	3746.5	95.0	748	PA2Y_MOUSE	P47713 mus musculu
5	3391	86.0	748	PA2Y_CHICK	P49147 gallus gall
6	2791	70.8	741	PA2Y_BRARE	P50392 brachydanio
7	232.5	5.9	649	PLB1_NORDE	O11121 torulaspora
8	221.5	5.6	612	PLB1_PENCH	P39437 penicillium
9	219.5	5.6	664	PLB1_YEAST	P39105 saccharomyc
10	207.5	5.3	706	PLB2_YEAST	O03674 saccharomyc
11	205.5	5.2	686	PLB3_YEAST	O08108 saccharomyc
12	148.5	3.8	536	SPO1_YEAST	P53541 saccharomyc
13	134	3.4	658	KPC1_YEAST	O25378 lytechinus
14	128	3.2	684	RP3A_RAT	P47709 rattus norv
15	125	3.2	704	RP3A_BOVIN	P06846 bos taurus
16	122.5	3.1	854	VG12_BPH2	P20345 bacterioph
17	122	3.1	3829	SACS_HUMAN	O9n214 homo sapien
18	118.5	3.0	664	YFGK_CAEEL	O18696 caenorhabdi
19	116.5	3.0	1216	P1B1_RAT	P10687 rattus norv
20	116	2.9	503	CP33_HUMAN	P05184 homo sapien
21	116	2.9	606	RP3A_MOUSE	P47708 mus musculu
22	116	2.9	1234	P1P3_MOUSE	P51432 mus musculu
23	115.5	2.9	1216	P1B1_BOVIN	P10894 bos taurus
24	115	2.9	970	T3RE_BPP1	P08764 bacterioph
25	113.5	2.9	1216	P1B1_HUMAN	O9nq66 homo sapien
26	113.5	2.9	3830	SACS_MOUSE	O9j1c8 mus musculu
27	112	2.8	2464	MAPR_MOUSE	P14873 mus musculu
28	111.5	2.8	697	KPCG_HUMAN	P01529 homo sapien
29	111.5	2.8	697	KPCG_RABIT	P10829 oryctolagus
30	111.5	2.8	854	VG12_BPP2A	P07537 bacterioph
31	111	2.8	1815	UN13_CAEEL	P27715 caenorhabdi
32	110.5	2.8	502	CP34_HUMAN	P08664 homo sapien
33	110.5	2.8	639	KPC1_DROME	P05130 drosophila

34	110.5	2.8	682	1	KPCG_BOVIN	P05128 bos taurus
35	108.5	2.8	422	1	SYT2_MOUSE	P46097 mus musculu
36	108.5	2.8	697	1	KPCG_MOUSE	P05697 mus musculu
37	108.5	2.8	1071	1	TRI_THEAC	P96086 thermoplasma
38	108	2.7	897	1	EP15_MOUSE	P42567 mus musculu
39	107.5	2.7	590	1	ASNS_ORYZA	O43011 oryza sativ
40	107	2.7	644	1	ARNT_DROME	O15945 drosophila
41	107	2.7	688	1	ARK2_RAT	P26819 rattus norv
42	107	2.7	1039	1	YLK6_CAEEL	P41954 caenorhabdi
43	106.5	2.7	543	1	APPA_BACSU	P42061 bacillus su
44	106	2.7	672	1	KPCG_HUMAN	P17252 homo sapien
45	106	2.7	1676	1	COS_HUMAN	P01031 homo sapien

ALIGNMENTS

RESULT	1	STANDARD	PRT	749 AA.
PA2Y_HUMAN				
ID	P47712			
AC	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE); LYSOPHOSPHOLIPASE (EC 3.1.1.5)].			
DE	PLA2G4 OR CPLA2.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OC	NCBI_TaxID=9606;			
OX	[1]			
RN	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RP	MEDLINE=91256305; PubMed=1904318; Ramasha C.S., Sultzman L.A., Clark J.D., Lin L.-L., Kriz R.W.,			
RA	Lin A.Y., Milona N., Knopf J.L.;			
RT	"A novel arachidonic acid-selective cytosolic PLA2 contains a Ca(2+)-dependent translocation domain with homology to PKC and GAP.";			
RL	Cell 65:1043-1051(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91331987; PubMed=1869522;			
RA	Sharp J., White D., Chlou G., Goodson T., Gamboa G., McClure D., Burgess S., Hoskins J., Skatrud P., Sportsman J., Becker G., Kang L., Roberts E., Kramer R.;			
RT	"Molecular cloning and expression of human Ca(2+)-sensitive cytosolic phospholipase A2.";			
RL	J. Biol. Chem. 266:14850-14853(1991).			
RN	[3]			
RP	MUTAGENESIS OF SER-505, AND PHOSPHORYLATION BY MAP KINASE.			
RX	MEDLINE=93145328; PubMed=8381049;			
RA	Lin L.-L., Wartmann M., Lin A.Y., Knopf J.L., Seh A., Davis R.J.;			
RT	"CPLA2 is phosphorylated and activated by MAP Kinase.";			
RL	Cell 72:269-278(1993).			
RN	[4]			
RP	MUTAGENESIS OF SER-228.			
RX	MEDLINE=9429545; PubMed=8027085;			
RA	Sharp J.D.,			
RT	Unpublished results, cited by:			
RL	Nalefski E.A., Sultzman L.A., Martin D.M., Kriz R.W., Towler P.S., Knopf J.L., Clark J.D.;			
RL	J. Biol. Chem. 269:18239-18249(1994).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 16-141.			
RX	MEDLINE=98104145; PubMed=9430701;			
RA	Pearl O., Fong S., Lynch D.E., Bycroft M., Williams R.L.;			
RT	"Crystal structure of a calcium-phospholipid binding domain from cytosolic phospholipase A2.";			
RL	J. Biol. Chem. 273:1596-1604(1998).			
RN	[6]			
RP	STRUCTURE BY NMR OF 1-138.			
RX	MEDLINE=98332749; PubMed=9665851;			

RA Xu G.-Y., McDonagh T., Yu H.-A., Nalefski E.A., Clark J.D.,
RA Cumming D.A.;
RT *Solution structure and membrane interactions of the C2 domain of
RT cytosolic phospholipase A2.";
RL J. Mol. Biol. 280:485-500(1998).
CC -1- FUNCTION: SELECTIVELY HYDROLYZES ARACHIDONYL PHOSPHOLIPIDS IN THE
CC SN-2 POSITION RELEASING ARACHIDONIC ACID. TOGETHER WITH ITS
CC LYSOPHOSPHOLIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF
CC THE INFLAMMATORY RESPONSE.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O - 1-ACYLGLYCERYL-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O - GLYCERO-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ATP, EGF,
CC THROMBIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. TRANSLOCATES TO MEMBRANE
CC VESICLES IN A CALCIUM-DEPENDENT FASHION.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS TISSUES SUCH AS
CC MACROPHAGES, PLATELETS, NEUTROPHILS, FIBROBLASTS AND LUNG
CC ENDOTHELIUM.
CC -1- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID
CC MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE
CC ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF
CC CYTOSOLIC CA2+.
CC -1- PTM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M72393; AAB0789.1; -;
DR EMBL: M68874; AAB60105.1; -;
DR PIR: A39329; A39329.
DR PDB: 1RLM; 25-FEB-98.
DR PDB: 1BC1; 13-JAN-99.
DR MIM: 600522; -;
DR InterPro: IPR000008; -;
DR InterPro: IPR002642; -;
DR Pfam: PF00168; C2; 1.
DR Pfam: PF01735; PLA2_B; 1.
DR PROSITE: PS50004; C2_DOMAIN_2; 1.
DR KW Hydrolyase; Lipid degradation; Calcium; Phosphorylation; 3D-structure.
FT DOMAIN 1 178 PHOSPHOLIPID BINDING (PROBABLE).
FT MOD_RES 505 505 C2 DOMAIN.
FT MOD_RES 505 505 PHOSPHORYLATION (BY MAPK).
FT MUTAGEN 228 228 S->A: ABOLISHES BOTH PHOSPHOLIPASE AND
FT LYSOPHOSPHATASE ACTIVITY.
FT MUTAGEN 505 505 S->A: DECREASES AGONIST-STIMULATED
FT RELEASE OF ARACHIDONIC ACID.
SQ SEQUENCE 749 AA; 85210 MW; 9F9CDD3A98231C70 CRC64;

Query Match 100.0%; Score 3942; DB 1; Length 749;
Best Local Similarity 100.0%; Pred. No. 3,1e-276;
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFIDYQHIIIEHOYSKFTVVVLRATVTKGAFGMDLTPDPYVLEFISTPDSRKRT 60
DB 1 MSFIDYQHIIIEHOYSKFTVVVLRATVTKGAFGMDLTPDPYVLEFISTPDSRKRT 60
QY 61 RHFNNDINVMNTEFEFIIDPNQENLETTLDANTVDELTGATFTVSSMKVGEKKEY 120
DB 61 RHFNNDINVMNTEFEFIIDPNQENLETTLDANTVDELTGATFTVSSMKVGEKKEY 120
QY 121 PFIENQVTEVLEMSLEVCSPDLRFSMALCDQEKTFROORKEHRESMKKLGPKNSEG 180
DB 121 PFIENQVTEVLEMSLEVCSPDLRFSMALCDQEKTFROORKEHRESMKKLGPKNSEG 180

QY 181 LHSARDVPVVAIIIGSGGFRAMVGFSGVAKALYESIILDCATYVAGLSGSTWYMTLSYH 240
DB 181 LHSARDVPVVAIIIGSGGFRAMVGFSGVAKALYESIILDCATYVAGLSGSTWYMTLSYH 240
QY 241 PDPPEKGPEINDELMKNSHNPLLLITQKKRYVESLMKKSSGQPTFFDIDGMLIG 300
DB 241 PDPPEKGPEINDELMKNSHNPLLLITQKKRYVESLMKKSSGQPTFFDIDGMLIG 300
QY 301 ETLIHRNMTTISLKEKYNTPACPLPTFCGLHVPRDVSLELFADWVEPSPEIGMAKYG 360
DB 301 ETLIHRNMTTISLKEKYNTPACPLPTFCGLHVPRDVSLELFADWVEPSPEIGMAKYG 360
QY 361 TFMAPDLFGSKFFMGTVKKYEENPLHFLMGVGSFSLFNRLVGVSGSGSGSTMEEB 420
DB 361 TFMAPDLFGSKFFMGTVKKYEENPLHFLMGVGSFSLFNRLVGVSGSGSGSTMEEB 420
QY 421 LENTTKHIVNDSDDSDSHKPTGKTEEDAGSDQSNQASWIRMTALVDSALFN 480
DB 421 LENTTKHIVNDSDDSDSHKPTGKTEEDAGSDQSNQASWIRMTALVDSALFN 480
QY 481 TREGRAKYHNFMGLNLTSTYPLSPDPAFQDSFDDDELDAVADPDEFERIYEDLV 540
DB 481 TREGRAKYHNFMGLNLTSTYPLSPDPAFQDSFDDDELDAVADPDEFERIYEDLV 540
QY 541 KSKKHIVVDSGLTFNLPYLLIRPQGVDLISFDSARPSSPPFKLLAEKMAKN 600
DB 541 KSKKHIVVDSGLTFNLPYLLIRPQGVDLISFDSARPSSPPFKLLAEKMAKN 600
QY 601 KLPFPKIDYVDREGKCYVFKPKNPMEKDCPTIHFLVLANINFRKYKAPGRETE 660
DB 601 KLPFPKIDYVDREGKCYVFKPKNPMEKDCPTIHFLVLANINFRKYKAPGRETE 660
QY 661 EEKEIADFIDPDSESPFTFNQVPCAFKRLHDMHNTLNIDVIEKAAVESIEYRR 720
DB 661 EEKEIADFIDPDSESPFTFNQVPCAFKRLHDMHNTLNIDVIEKAAVESIEYRR 720
QY 721 QNPSRCSVLSNVEARFENKEFLSKPKA 749
DB 721 QNPSRCSVLSNVEARFENKEFLSKPKA 749

RESULT 2
PASY_HORSE
ID PASY_HORSE STANDARD: PRT: 749 AA.
AC 077793;
DT 15-JUL-1999 (Rel. 38, last sequence update)
DT 15-JUL-1999 (Rel. 38, last sequence update)
DT 15-JUL-1999 (Rel. 38, last sequence update)
DE CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) (INCLUDES: PHOSPHOLIPASE A2
DE (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE);
DE LYSOPHOSPHOLIPASE (EC 3.1.1.5)).
GN PLA2G4 OR CPLA2.
OS Equus caballus (horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC NCBI_Taxid=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Neutrophils;
RA Larsson Forsell P.K.A., Lindberg A., Karlsson S., Lindgren J.A.,
RA Claesson H.-E.;
RT "Purification, characterization and cDNA sequencing of calcium-
RT dependent cytosolic phospholipase A2 from equine neutrophils.";
RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: SELECTIVELY HYDROLYZES ARACHIDONYL PHOSPHOLIPIDS IN THE
CC SN-2 POSITION RELEASING ARACHIDONIC ACID. TOGETHER WITH ITS
CC LYSOPHOSPHOLIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF
CC THE INFLAMMATORY RESPONSE.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O - 1-ACYLGLYCERYL-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O - GLYCERO-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ATP, EGF,

THROMBIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+ (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: CYTOPLASMIC. TRANSLOCATES TO MEMBRANE VESICLES IN A CALCIUM-DEPENDENT FASHION (BY SIMILARITY).

-1- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF CYTOSOLIC CA2+ (BY SIMILARITY).

-1- PTM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE (BY SIMILARITY).

-1- SIMILARITY: CONTAINS 1 C2 DOMAIN.

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CC EMBL: AF092539; AAC61774.1; -

DR InterPro: IPR000008; -

DR InterPro: IPR002642; -

DR Pfam: PF00168; C2; 1.

DR Pfam: PF01735; PLA2_B; 1.

DR PROSITE: PS50004; C2_DOMAIN_2; 1.

KM Hydrolyase; lipid degradation; calcium; phosphorylation.

FT DOMAIN 1 178 PHOSPHOLIPID BINDING (PROBABLE).

FT MOD_RES 5 106 C2 DOMAIN.

FT MOD_RES 505 505 PHOSPHORYLATION (BY MADK) (BY SIMILARITY).

SEQUENCE 749 AA; 85454 MW; 493A67DF28D50FE0 CRC64;

Query Match 96.2%; Score 3793; DB 1; Length 749;

Best Local Similarity 95.3%; Pred. No. 1.7e-265;

Matches 744; Conservative 24; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSFTIDYQHIIVEHOXSHKFTVVVLRATKYKAFGMDLTPPYVELFISTTPDSKRT 60

DB 1 MSFTIDYQHIIVEHOXSHKFTVVVLRATKYKAFGMDLTPPYVELFISTTPDSKRT 60

QY 61 RHFNNDINPVWNETFEFLDPNOENVLEITLMDANYMDETLGTATFTVSSMKGKREY 120

DB 61 RHFNNDINPVWNETFEFLDPNOENVLEITLMDANYMDETLGTATFTVSSMKGKREY 120

QY 121 PFTFNQVTEVWLEMSLEVSCPDLRFSMALCDEKTPROQRKHIRSMKKLLGPKRSEG 180

DB 121 PFTFNQVTEVWLEMSLEVSCPDLRFSMALCDEKTPROQRKHIRSMKKLLGPKRSEG 180

QY 181 LHSARDVPVVAIIIGSGGFRAHYGSGVMKALYESGILDCATYVAGLSGTWYSTLYSH 240

DB 181 LYSTRDVPVVAIIIGSGGFRAHYGSGVMKALYESGILDCATYVAGLSGTWYSTLYSH 240

QY 241 PDPEPEGEPEINEELKKNVSHNPLLLTPQVKRYVESLMKKKSGQVPTFDIFGMLIG 300

DB 241 PDPEPEGEPEINEELKKNVSHNPLLLTPQVKRYVESLMKKKSGQVPTFDIFGMLIG 300

QY 301 ETLIHRNMNTLSLKEKVTACQPLFTCLHYKPPVSELMFADWVEFSPEYEGMAKYG 360

DB 301 ETLIHRNMNTLSLKEKVTACQPLFTCLHYKPPVSELMFADWVEFSPEYEGMAKYG 360

QY 361 TFMAPDLFGSKFPMGTGVKKYEENPLHFLMGVGSASFILFNRYLGVSGSQSRGSTMEEE 420

DB 361 TFMAPDLFGSKFPMGTGVKKYEENPLHFLMGVGSASFILFNRYLGVSGSQSRGSTMEEE 420

QY 421 LENTTKHIVYNDSDSDSHPEPKGTENDAGSDYOSDNQASHIRMAIYVSDSALFN 480

DB 421 LENTTKHIVYNDSDSDSHPEPKGTENDAGSDYOSDNQASHIRMAIYVSDSALFN 480

QY 481 TRGGRAGKVNFMGLNLMNYSPLSDFAQDSFDDDLDAVAVDPDEFERYEPLDY 540

DB 481 TRGGRAGKVNFMGLNLMNYSPLSDFAQDSFDDDLDAVAVDPDEFERYEPLDY 540

QY 541 KSKKIHVDSGLTFENLPYLILRPORCVDLISFDSARPSSDPPKELLAEKNAKM 600

DB 541 KSKKIHVDSGLTFENLPYLILRPORCVDLISFDSARPSSDPPKELLAEKNAKM 600

QY 601 KLPEPKIDPVYDFREGIEKCYVERKPKNDMEKDCPTIIHFVLINIRKRYKAGVPRETE 660

DB 601 KLPEPKIDPVYDFREGIEKCYVERKPKNDMEKDCPTIIHFVLINIRKRYKAGVPRETE 660

QY 661 EKEEIAFDLFDDEPSEFSFTFNQYPMQAKRLHDLHFNTLNNIDYIKAMVESIEYR 720

DB 661 EKEEIAFDLFDDEPSEFSFTFNQYPMQAKRLHDLHFNTLNNIDYIKAMVESIEYR 720

QY 721 QNPSRCVSLSNVEARFNFKEFLSKPKA 749

DB 721 QNPSRCVSLSNVEARFNFKEFLSKPKA 749

RESULT 3

PAZY_RAT PAZY_RAT STANDARD; PRT; 752 AA.

ID P50393;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE); DE LYSOPHOSPHOLIPASE (EC 3.1.1.5)].

GN PLA2G4 OR CPLA2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_Taxid=10116;

OX [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Brain;

RC Owada Y., Tomioka T., Yoshimoto T., Kondo H.;

RT "Molecular cloning of rat cDNA for cytosolic phospholipase A2 and the increased gene expression in the dentate gyrus following transient forebrain ischemia."

RT Brain Res. Mol. Brain Res. 25:364-368(1994).

RN [2]

RP ERRATUM.

RC MEDLINE=95206125; PubMed=7898324;

RA Owada Y., Tomioka T., Yoshimoto T., Kondo H.;

RL Brain Res. Mol. Brain Res. 27:355-355(1994).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Pancreatic Islets;

RA Ma Z., Ramanadham S., Hu Z., Turk J.;

RT MEDLINE=98223459; PubMed=9555100;

RT "Cloning and expression of a group IV cytosolic Ca2+-dependent phospholipase A2 from rat pancreatic islets. Comparison of the expressed activity with that of an islet group VI cytosolic Ca2+-independent phospholipase A2."

RT Biochim. Biophys. Acta 1391:384-400(1998).

RL -1- FUNCTION: SELECTIVELY HYDROLYZES ARACHIDONYL PHOSPHOLIPIDS IN THE SN-2 POSITION RELASING ARACHIDONIC ACID. TOGETHER WITH ITS LYSOPHOSPHOLIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF THE INFLAMMATORY RESPONSE.

CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O - 1-ACYLGLYCERYL-PHOSPHOCHOLINE + A FATTY ACID ANION.

CC -1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O = GLYCERO-PHOSPHOCHOLINE + A FATTY ACID ANION.

CC -1- ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ATP, EGF, THROMBIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. TRANSLOCATES TO MEMBRANE VESICLES IN A CALCIUM-DEPENDENT FASHION (BY SIMILARITY).

CC -1- TISSUE SPECIFICITY: IN BRAIN TISSUE, EXPRESSED IN LOW LEVELS IN OLFACTORY MITRAL AND GRANULE CELLS, IN HIPPOCAMPAL PYRAMIDAL CELLS AND IN DENTATE AND CEREBELLAR GRANULE CELLS.

CC -1- INDUCTION: LEVELS OF RAT CPLA2 ARE INCREASED IN DENTATE GRANULE CELLS DURING ISCHEMIA.

CC -1- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID
 CC MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE
 CC ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF
 CC CYTOSOLIC CA2+ (BY SIMILARITY).
 CC -1- PTM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: S78829; AAB33847.1; -
 CC EMBL: U38376; AAC21591.1; -
 CC HSSP: P47712; IBCI.
 CC InterPro: IPR000008; -
 CC InterPro: IPR002642; -
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF01735; PLA2_B; 1.
 CC PROSITE: P55004; C2_DOMAIN_2; 1.
 CC HydroLase: Ldbid degradation; Calcium; phosphorylation.
 CC KIR DOMAINS 1 178 PHOSPHOLIPID BINDING (PROBABLE).
 CC FT DOMAIN 5 106 C2 DOMAIN.
 CC FT MOD_RES 505 505 PHOSPHORYLATION (BY MAPK) (BY
 CC SIMILARITY)
 CC FT CONFLICT 139 139 C -> S (IN REF. 3).
 CC FT CONFLICT 159 159 R -> Q (IN REF. 3).
 CC FT CONFLICT 287 287 Q -> L (IN REF. 3).
 CC FT CONFLICT 308 310 MST -> IYP (IN REF. 3).
 CC FT CONFLICT 410 410 S -> L (IN REF. 3).
 CC FT CONFLICT 489 489 E -> V (IN REF. 3).
 CC FT CONFLICT 635 635 P -> T (IN REF. 3).
 CC FT CONFLICT 752 AA; 85706 MW; C68F71HB05FBF732 CRC64;
 SQ SEQUENCE

Query Match 95.2%; Score 3752; DB 1; Length 752;
 Best Local Similarity 94.5%; Pred. No. 1.5e-262;

Matches 708; Conservative 24; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSFIDYOHIIYEHQYSHKFTVVVLRATVTKGAFGMDLTPPYVELFISTPDSRRKT 60
 DB 1 MSFIDYOHIIYEHQYSHKFTVVVLRATVTKGAFGMDLTPPYVELFISTPDSRRKT 60
 QY 61 RHNNDINPVNMTFFELIDPNOENVLEITLDANYMDELTGATFVYSMAKVGEEKY 120
 DB 61 RHNNDINPVNMTFFELIDPNOENVLEITLDANYMDELTGATFVYSMAKVGEEKY 120
 QY 121 PTFNNOVTEVLEMSLEVCSCPLRFSMALCDEKTFROORKEHIESMKKLGPNSKE 180
 DB 121 PTFNNOVTEVLEMSLEVCSCPLRFSMALCDEKTFROORKEHIESMKKLGPNSKE 180
 QY 181 LHSARDVPAVALIGSGGFRAMVFGSVKALYESGILDCATYVAGLSGSTMVSTLYSH 240
 DB 181 LYSTRDVPAVALIGSGGFRAMVFGSVKALYESGILDCATYVAGLSGSTMVSTLYSH 240
 QY 241 PDPEPGPEEINELMKNSHNPILLITPOKARYYESLMKKSSQOPVTFDIFGMLIG 300
 DB 241 PDPEPGPEEINELMKNSHNPILLITPOKARYYESLMKKSSQOPVTFDIFGMLIG 300
 QY 301 ETLIHRMNTTSLLEKXNTAQCPLPLFTCLHVKPDVSELMADWVERSPYEIGMAKYG 360
 DB 301 ETLIHRMNTTSLLEKXNTAQCPLPLFTCLHVKPDVSELMADWVERSPYEIGMAKYG 360
 QY 361 TEWAPDLFGSKFPMGTIVVKYEENPLHFLMGVGSASFILFNVLVSGSOSRGSTMEEE 420
 DB 361 TEWAPDLFGSKFPMGTIVVKYEENPLHFLMGVGSASFILFNVLVSGSOSRGSTMEEE 420
 QY 421 LENTITKHIVSNDSSDDESHPEPKGTENEDAGSDYQSDNQASWIRHMTALVSDSALFN 480
 DB 421 LENTITKHIVSNDSSDDESHPEPKGTENEDAGSDYQSDNQASWIRHMTALVSDSALFN 480

DB 421 LENTITKHIVSNDSSDDESHPEPKGTENEDAGSDYQSDNQASWIRHMTALVSDSALFN 480
 QY 481 TREGRAGVHNEMGLNLTNTSYPLSPDFAOTQSDFDDDELDAVAADPEFERIYEDLV 540
 DB 481 TREGRAGVHNEMGLNLTNTSYPLSPDFAOTQSDFDDDELDAVAADPEFERIYEDLV 540
 QY 541 KSKKHIVDVGSLFNPILPYLLIRPQGVLDLISFDSARPSSDPPPEKLLAEKMAKN 600
 DB 541 KSKKHIVDVGSLFNPILPYLLIRPQGVLDLISFDSARPSSDPPPEKLLAEKMAKN 600
 QY 601 KLPFKRIDYVDRDLKCYCYEKKRPNPMKDCPTIHFVLANTNFRKRYKAPVRETE 660
 DB 601 KLPFKRIDYVDRDLKCYCYEKKRPNPMKDCPTIHFVLANTNFRKRYKAPVRETE 660
 QY 661 EEKEIDFIDFDDPESPSTFNNQYPNQAFKRLHMLHFNLTNIDVIEKAVESIEYRR 720
 DB 661 EEKEIDFIDFDDPESPSTFNNQYPNQAFKRLHMLHFNLTNIDVIEKAVESIEYRR 720
 QY 721 QNPSRCSVSLSNVEARFENKEFLSKPKA 749
 DB 721 QNPSRCSVSLSNVEARFENKEFLSKPKA 749

RESULT 4
 PAZY_MOUSE
 ID PAZY_MOUSE STANDARD; PRT; 748 AA.
 AC P47713;
 DT 01-FEB-1996 (rel. 33; Last sequence update)
 DT 15-JUL-1999 (rel. 38; Last annotation update)
 DE CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2
 DE (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE);
 GN LYSOPHOSPHOLIPASE (EC 3.1.1.5)].
 OS PLA2G4 OR CPLA2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91256305; PubMed=1904318;
 RA Clark J.D., Lin L.-L., Kitz R.W., Ramesha C.S., Soltzman L.A.,
 RA Lin A.Y., Milona N., Knopf J.L.;
 RT "A novel arachidonic acid-selective cytosolic PLA2 contains a Ca(2+)-
 RT dependent translocation domain with homology to PKC and GAP.";
 RL Cell 65:1043-1051(1991).
 CC -1- FUNCTION: SELECTIVELY HYDROLYZES ARACHIDONYL PHOSPHOLIPIDS IN THE
 CC SN-2 POSITION RELEASING ARACHIDONIC ACID. TOGETHER WITH ITS
 CC LYSOPHOSPHOLIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF
 CC THE INFLAMMATORY RESPONSE.
 CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O = GLYCERO-
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -1- ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ATP, EGF,
 CC THROMBIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. TRANSLOCATES TO MEMBRANE
 CC VESICLES IN A CALCIUM-DEPENDENT FASHION.
 CC -1- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID
 CC MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE
 CC ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF
 CC CYTOSOLIC CA2+ (BY SIMILARITY).
 CC -1- PTM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
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 CC -----

CC EMBL: M72394; AAB00796.1; -.
 DR HSSP: P47712; IBCI.
 DR MGI: 1195256; Pla2g4.
 DR InterPro: IPR000008; -.
 DR InterPro: IPR002642; -.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF01735; PLA2_B; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR HydroLase: Lipid degradation; Calcium; Phosphorylation.
 FT DOMAIN 1 178 PHOSPHOLIPID BINDING (PROBABLE).
 FT MOD_RES 505 106 C2 DOMAIN.
 FT MOD_RES 505 305 PHOSPHORYLATION (BY MARK) (BY
 SIMILARITY).
 SQ SEQUENCE 748 AA; 85222 MW; 49D12BB2911492A CRC64;

Query Match 95.0%; Score 3746.5; DB 1; Length 748;
 Best Local Similarity 94.8%; Pred. No. 3.8e-262;
 Matches 708; Conservative 24; Mismatches 14; Indels 1; Gaps 1;

QY 1 MSFIDPQHIIVEHQYSHKFTVYVLRATKYTKGAFGMDLPDPYVELFISTPDSRRRT 60
 |||||
 DB 1 MSFIDPQHIIVEHQYSHKFTVYVLRATKYTKGAFGMDLPDPYVELFISTPDSRRRT 60
 QY 61 RHFNNDINPVWNETFEELDPNENLEITLMDANYVDETLGATFTVSMKVGKREY 120
 |||||
 DB 61 RHFNNDINPVWNETFEELDPNENLEITLMDANYVDETLGATFTVSMKVGKREY 120
 QY 121 PFITNOTENVLEMSLVSCPDLPFSMALCDOKETROQKEIRRESMKLLQPKKSEC 180
 |||||
 DB 121 PFITNOTENVLEMSLVSCPDLPFSMALCDOKETROQKEIRRESMKLLQPKKSEC 180
 QY 121 PFITNOTENVLEMSLVSCPDLPFSMALCDOKETROQKEIRRESMKLLQPKKSEC 180
 |||||
 DB 121 PFITNOTENVLEMSLVSCPDLPFSMALCDOKETROQKEIRRESMKLLQPKKSEC 180
 QY 181 LHSARDPVVAIIIGSGGFRAMVGFSCVMKALYESGILDCATYAGLSGFTWYSTLYSH 240
 |||||
 DB 181 LYSRDVPAVAIIIGSGGFRAMVGFSCVMKALYESGILDCATYAGLSGFTWYSTLYSH 240
 QY 241 PDPEKPEEINELMKNVSHNPLLLTPOKKRYVESLWKKKSGQPVTFDFGMLIG 300
 |||||
 DB 241 PDPEKPEEINELMKNVSHNPLLLTPOKKRYVESLWKKKSGQPVTFDFGMLIG 300
 QY 301 ETLIHNMNTLSLKEKVMTAOCPLFTCLHYKPDVSELMFADWVEFSYEIGMAKYG 360
 |||||
 DB 301 ETLIHNMNTLSLKEKVMTAOCPLFTCLHYKPDVSELMFADWVEFSYEIGMAKYG 360
 QY 361 TFMAPDLFGSKFEMGTVYKKEENPLHFLMGVGSASFILFNRYLGVSGSNGKSTMEEE 420
 |||||
 DB 361 TFMAPDLFGSKFEMGTVYKKEENPLHFLMGVGSASFILFNRYLGVSGSNGKSTMEEE 420
 QY 421 LENTITHIVSNDSDSDSHKPGTENEDAGSDYOSDNOASWIRHIMALVSDSALFN 480
 |||||
 DB 421 LENTITHIVSNDSDSDSHKPGTENEDAGSDYOSDNOASWIRHIMALVSDSALFN 480
 QY 481 TREBRACKVNHFMGLNLSYPLSLDRATQSPDDELDAVAADPEERIEYEPIDV 540
 |||||
 DB 481 TREBRACKVNHFMGLNLSYPLSLDRATQSPDDELDAVAADPEERIEYEPIDV 540
 QY 541 KSKRIHVVDGLFNLPLRPGRGVDLISDFGSRPDSPPREKELLAKMAKN 600
 |||||
 DB 541 KSKRIHVVDGLFNLPLRPGRGVDLISDFGSRPDSPPREKELLAKMAKN 600
 QY 540 KSKRIHVVDGLFNLPLRPGRGVDLISDFGSRPDSPPREKELLAKMAKN 599
 |||||
 DB 540 KSKRIHVVDGLFNLPLRPGRGVDLISDFGSRPDSPPREKELLAKMAKN 599
 QY 601 KLPPKIDPVYFREGKECYVFKPKNPDMKDCPTIIHFVLANINFRKYKAPGVPRETE 660
 |||||
 DB 601 KLPPKIDPVYFREGKECYVFKPKNPDMKDCPTIIHFVLANINFRKYKAPGVPRETE 660
 QY 661 EEKRIAPDIFDDPESPFSTFNQYRPNQAKRLDLMLHFNLANIDVYKEMVSEIERR 720
 |||||
 DB 661 EEKRIAPDIFDDPESPFSTFNQYRPNQAKRLDLMLHFNLANIDVYKEMVSEIERR 720
 QY 721 QNPSRCSVLSNVEARFENKFLSKP 747
 |||||
 DB 721 QNPSRCSVLSNVEARFENKFLSKP 746
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RESULT 5
 PAZY CHICK STANDARD; PRT; 748 AA.
 ID PAZY CHICK
 AC PA9147;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2
 DE (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE);
 DE LYSOPHOSPHOLIPASE (EC 3.1.1.5)].
 GN PLA2G4 OR CPLA2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=94299545; PubMed=8027085;
 RA Nalefski E.A., Sultzman L.A., Martin D.M., Kriz R.W., Towler P.S.,
 RA Knopf J.L., Clark J.D.;
 RT "elination of two functionally distinct domains of cytosolic
 RT phospholipase A2, a regulatory Ca(2+)-dependent lipid-binding domain
 RT and a Ca(2+)-independent catalytic domain.";
 RL J. Biol. Chem. 269:18239-18249(1994).
 CC -1- FUNCTION: SELECTIVELY HYDROLYZES ARACHIDONYL PHOSPHOLIPIDS IN THE
 CC SN-2 POSITION RELEASING ARACHIDONIC ACID. TOGETHER WITH ITS
 CC LYSOPHOSPHOLIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF
 CC THE INFLAMMATORY RESPONSE.
 CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O = GLYCERO-
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -1- ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ATP, EGF,
 CC THROMBIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. TRANSLOCATES TO MEMBRANE
 CC VESICLES IN A CALCIUM-DEPENDENT FASHION (BY SIMILARITY).
 CC -1- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID
 CC MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE
 CC ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF
 CC CYTOSOLIC CA2+ (BY SIMILARITY).
 CC -1- PTM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.

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CC EMBL: U10329; AAA53228.1; -.
 DR HSSP: P47712; IBCI.
 DR InterPro: IPR000008; -.
 DR InterPro: IPR002642; -.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF01735; PLA2_B; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR HydroLase: Lipid degradation; Calcium; Phosphorylation.
 FT DOMAIN 1 178 PHOSPHOLIPID BINDING.
 FT MOD_RES 505 106 C2 DOMAIN.
 FT MOD_RES 505 305 PHOSPHORYLATION (BY MARK) (BY
 SIMILARITY).
 SQ SEQUENCE 748 AA; 84978 MW; 996A5256CA032F75 CRC64;

Query Match 86.0%; Score 3391; DB 1; Length 748;
 Best Local Similarity 83.9%; Pred. No. 1.5e-236;
 Matches 625; Conservative 64; Mismatches 56; Indels 0; Gaps 0;

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RA Nalefski E.A., Sulteman L.A., Mattlin D.M., Kitz R.W., Towler P.S.,
RT Knopf J.L., Clark J.D.:
CC "Definition of two functionally distinct domains of cytosolic
CC phospholipase A2, a regulatory Ca(2+)-dependent lipid-binding domain
CC RT and a Ca(2+)-independent catalytic domain".
RL J. Biol. Chem. 269:18239-18249(1994).
CC -1- FUNCTION: SELECTIVELY HYDROLYZES ARACHIDONYL PHOSPHOLIPIDS IN THE
CC SN-2 POSITION RELEASING ARACHIDONIC ACID. TOGETHER WITH ITS
CC LYOPHOPHO-LIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF
CC THE INFLAMMATORY RESPONSE.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGlyceryl-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O = GLYCERO-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ADP, EGf,
CC THROMBIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. TRANSLOCATES TO MEMBRANE
CC VESICLES IN A CALCIUM-DEPENDENT FASHION (BY SIMILARITY).
CC -1- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID
CC MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE
CC ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF
CC CYTOSOLIC CA2+ (BY SIMILARITY).
CC -1- PTM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE (BY
CC SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
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CC
CC EMBL: U10330; AAA53229.1; -.
DR HSSP: P47712; 1BC1.
DR ZFIN: ZDB-GENE-980415-45; cpla2.
DR InterPro: IPR000008; -.
DR InterPro: IPR002642; -.
DR Pfam: PF00168; C2_1.
DR Pfam: PF01735; PLA2_B; 1.
DR PROSITE: PS50004; C2 DOMAIN_2; 1.
KW Hydrolase; Lipid degradation; Calcium; Phosphorylation.
KT DOMAIN 1 172 PHOSPHOLIPID BINDING (PROBABLE).
FT DOMAIN 1 100 C2 DOMAIN.
FT FT 498 498 PHOSPHORYLATION (BY MAPK) (BY
FT MOD_RES 498 498 SIMILARITY).
SQ SEQUENCE 741 AA; 83809 MM; 34896BIAB364A9D4 CRC64;

Query Match 70.8%; Score 2791; DB 1; Length 741;
Best Local Similarity 72.7%; Pred. No. 2.5e-193;
Matches 537; Conservative 81; Mismatches 111; Indels 10; Gaps 7;

9 HITVEHQSHKRVTVVLAATKYTKGAFGMGLDTPPYVELFSTYPSDKSRKRHRHNNDIN 68
QY ::::||||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 3 NIIVGHQVSHRKLVVAENVTAKAFGLDLDPPIYELSPVTLPESKRRRIHNNDIN 62

69 PAVNNEFFFIILDPOENVLETITMDANYVMDELTGTATFYTSMAKVYGEKEVPVFNFQYT 128
QY ::::||||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 63 PAVNNEFFFIILDPONSNVLEYITLMADANYVMDETITAKTSLSKLVAOMEHNTLSIGRTT 122

129 EVVLMSLSEVCSCPLRFSMLCDEKFEPBOORCKHIRSMKKLLGPKNSEGSLHA-BDV 187
QY ::::||||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 123 KVFILLLEVCASTDLRSMILCODEKLFMQTRDRVMISIKLLKMENPRELPSSPREV 182

188 PVVALIGSGGGFRANVGSGVKALKALYESGILDCAITYVAGLSGSTWYMSLTLYSHDPPEKG 247
QY ::::||||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 183 PLIALIGSGGGFRANVGSGVKALKALYESGVFCATYYVAGLSGSTWYMSLTLYSHPEPAKG 242

248 PEINIEELMKVSNHPDLLLPQAKKRYVESIMKSSGCGPTTFIDIGMLIGETLINNR 307
QY ::::||||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 243 PGDIKKELMNRSNPDLKLIPONTNIRVVKALKMKKSAGOPTTFIDIGMLIGETLINBGR 302

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Query Match	5.68;	Score 219.5;	DB 1;	Length 664;
Best Local Similarity	20.28;	Pred. No. 3.8e-08;		
Matches 137;	Conservative 98;	Mismatches 223;	Indels 221;	Gaps 31;

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OY      678 ESTEFENQACRHLHMDLNTNNDVLRKEAVES-----LEY 718
Db       505 NSRSHFNCNOSTFK-----MSYSDSERGMKTNKGFEATMGFTDDSDPLGCVCAITRR 559
OY      719 BRON-----PSRCSVSLSN 732
Db       560 KQNINMNLALPSECSCCFYN 578

RESULT 10
ID     PLB2_YEAST          STANDARD;           PRT;         706 AA.
AC    003674;
DT    01-NOV-1997 (Rel. 35, Created)
DT    01-NOV-1997 (Rel. 35, Last sequence update)
DT    01-OCT-2000 (Rel. 40, Last annotation update)
DE    LYSOPHOSPHOLIPASE 2 PRECURSOR (EC 3.1.1.5) (PHOSPHOLIPASE B 2).
GN     PLB2 OR YMR006C OR YM8270.0bc.
OS     Saccharomyces cerevisiae (Baker's yeast).
OC     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC     Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX     NCBI_Taxid=4932;
RN     [1]
RP     SEQUENCE FROM N.A.
RC     STRAIN=S288C / AB972;
RA     Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL     Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RM     [2]
RN     SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC     STRAIN=DG338;
RX     MEDLINE=99249797; Pubmed=10231538;
RY     Fryst H., Oskoulian B., Kuypers F.A., Saba J.D.;
RT     "The PLB2 gene of Saccharomyces cerevisiae confers resistance to
RT     lysophosphatidylcholine and encodes a phospholipase
RL     B/lysophospholipase." ;
RL     Biochemistry 38:5864-5871(1999).
CC     -I- FUNCTION: CATALYZES THE RELEASE OF FATTY ACIDS FROM
CC     LYSOPHOSPHOLIPIDS. SHOWS LYSOPHOSPHOLIPASE ACTIVITY TOWARD
CC     LYSOPHOSPHATIDYLCHOLINE, LYSOPHOSPHATIDYLSERINE, AND
CC     LYSOPHOSPHATIDYLETHANOLAMINE.
CC     CC
CC     -I- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H2O =
CC     GLYCEROPHOSPHOCHOLINE + A FATTY ACID ANION.
CC     CC
CC     -I- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
CC     CC
CC     -I- SIMILARITY: TO OTHER FUNGAL LYSOPHOSPHOLIPASES AND TO YEAST
CC     SPOL.
CC     -----
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CC     or send an email to license@isb-sib.ch).
CC     -----
DR     EMBL; Z48613; CAAB8521.1; -.
DR     EMBL; AF129165; AAD28616.1; -.
DR     SGD; S0004608; PLB2
DR     InterPro; IPR002642; .
KW     Pfam; PF01735; PLA2_B; 1.
KW     Lipid degradation; Hydrolase; Glycoprotein; Signal.
FT     SIGNAL                      ?
FT     CHAIN                       ?
FT     DOMAIN                     657..667
FT     POLY-SER.                  POLY-SER.
FT     POLY-ASP.                  POLY-ASP.
FT     DOMAIN                     671..674
FT     POLY-SER.                  POLY-SER.
FT     CARBOHYD                   47..47
FT     N-LINKED (GLCNAG. . . )   (POTENTIAL).
FT     CARBOHYD                   80..80
FT     N-LINKED (GLCNAG. . . )   (POTENTIAL).
FT     CARBOHYD                   94..94
FT     N-LINKED (GLCNAG. . . )   (POTENTIAL).
FT     CARBOHYD                   125..125
FT     N-LINKED (GLCNAG. . . )   (POTENTIAL).
FT     CARBOHYD                   162..162
FT     N-LINKED (GLCNAG. . . )   (POTENTIAL).
FT     CARBOHYD                   181..181
FT     N-LINKED (GLCNAG. . . )   (POTENTIAL).
FT     CARBOHYD                   193..193
FT     N-LINKED (GLCNAG. . . )   (POTENTIAL).

```

```

FT CAROHD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 491 491 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 524 524 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 543 543 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 567 567 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 584 584 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 598 598 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 630 630 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 642 642 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 652 652 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CAROHD 658 658 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 706 AA: 75455 MW; 5E7BF22C7780DC2 CRC64;

```

Query Match 5.3% Score 207.5; DB 1: Length 706;
 Best Local Similarity 21.1%; Pred. No. 3e-07;
 Matches 118; Conservative 100; Mismatches 195; Indels 147; Gaps 28;

```

QY 138 VCSQD-----LRFSMALCDOEKTEPROQRKEHRESMKKLGLPKNS-----EGLHSA 184
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 34 IIPCSDDTSLVRNMSGSTAEFDMLKRRDAYTKALHSLFSLNATSNFSDTSLSTLFS 93
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 185 R-DVPAVALILSGGGRAMVGSVGMALYE-----SGILDCATYVAGLSGSW 232
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 94 NSSNPKEIGIASGGGYRMLAGAGMIAMDRKTDGANEHGLGLSSTYSLSGGGMW 153
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 233 YMSLT-YSHPDPEKPEPEINE-ELMKNVSH--NP---LLLTPOKVRVESLMMKKS 284
   ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 154 LFTGLANNTVSVQELVDHMSSESDTAMITKSTLVNPGSNLYTTERMESIVQEOAKSD 213
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 285 SCQPVTFDFIGMLIGETLIHNRMT-----TLSSLK-EKVNTAQCPLPFLCHVKPDV 338
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 214 AGFNISLSDLMRALSYNFPSPDAGSALTWLSLSDVDVFNKNGEMRLPITVADGKPGT 273
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 339 SEL-HEADVESPYEIGMAKGTGMADPLFGSKFPKGTIVVKKYEEBNPLFLMGWGSFAF 397
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 274 TYININATLFEETPE-----NVTNGKPVNKQCVS-----GYDN-AG--- 329
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 398 SLTFN-RVLGVSGSGRSTMEELNITTKHIVNSDSDSDSHSPKTEHDAQSGY 456
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 298 NAFDVKYIGT-----NVTNGKPVNKQCVS-----GYDN-AG--- 329
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 457 QSDNQASWIRHIMALVSDSALFNTREGRAKVHNFMLGINTSYLSPLSDFATQD-- 514
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 330 -----FVIATASLFN-----EFSLEASTSTYKM--INSPANKYVN 364
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 515 --SFDDDELDAVADP--DER-ERYEPLDYKSKTIHVDGLT-FNLPYLLRPORG 567
   ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 365 NLSQDDDDLAIAANPFXKTEVDNRVYTSIYDADDLFVLDGDEQDNPLPLVLIKKED 424
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 568 VDLITSFDSARPSSSP--FKELLAKMAKMK-LPEPKI-DRPYVDRGLKCYAF 623
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 425 LDVVALDLSMDTDESMPGVCMTNTEKQYKQKGMAFYPVPDVNTLNLGTLKKPTF 484
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 624 ---KPKN-PDMKDCPTI 639
   ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 485 FCGDAKNLTDEYIPPLYV 504

```

RESULT 11
 PLB3_YEAST STANDARD; PRT; 686 AA.
 AC 008108;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)

```

DE PUTATIVE LYSOPOHOPHOLIPASE PRECURSOR (EC 3.1.1.5) (PHOSPHOLIPASE B).
GN YOLO11W.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_Taxid=4932;
RN [1]
RP Hughes B., Pohl T.M.;
RL Submitted (Jul-1996) to the EMBL/Genbank/DBJ databases.
CC - FUNCTION: CATALYZES THE RELEASE OF FATTY ACIDS FROM
CC LYSOPOHOPHOLIPIDS.
CC - CATALYTIC ACTIVITY: 2-LYSOPOHOPHATIDYLCHOLINE + H(2)O =
CC GLYCEROPHOSPHOCHOLINE + A FATTY ACID ANION.
CC - SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
CC - SIMILARITY: TO OTHER FUNGAL LYSOPOHOPHOLIPASES AND TO YEAST
CC SPOI.
CC -----
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CC -----
DR EMBL: 274753; CAA99010.1; .
DR SGD: S0005371; YOLO11W.
DR InterPro: IPR002642; .
DR Pfam: PF01735; PLA2_B; 1.
KW Hypothetical protein; Lipid degradation; Hydrolase; glycoprotein;
KW signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 686 PUTATIVE LYSOPOHOPHOLIPASE.
FT DOMAIN 627 643 POLY-SER.
FT CARBOHD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 519 519 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 547 547 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 588 588 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 686 AA: 75076 MW; 95A2DBF41BF3E20F CRC64;

```

Query Match 5.2% Score 205.5; DB 1: Length 686;
 Best Local Similarity 22.2%; Pred. No. 4.1e-07;
 Matches 139; Conservative 99; Mismatches 186; Indels 203; Gaps 38;

```

QY 140 SCDP-----LRFSMALCDOEKTEPROQRKE-----HIESMKKLGLPKN 177
   ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 39 SCPDQNLNLRKATSTSONSAMLKRNKTVSALKDFLTRATNPSDSSEVSKLFNCGN 98
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 178 SGLHSARDVPVAILIGSGGFRAMVGSVGMAL-----YE---SGILDCATYVAGL 227
   ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 99 SENL-----PKIAVAVSGGYRSMLTGAGVLAAMDRTEGAYEHGLGLSTYVLSGA 152
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 228 SGSTWMTLYSHPDPEKPEPEIN-----ELMKNVSHNPL-----LTP-----Q 270
   ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 153 SGGNMLVGTL-----ALNNMTSVQDILNNMNDOSIMWLSISVTPGGINIFK 200
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 271 KYKRY-----VESLWKKKSGQPVTFDFIGMLTG-----ETLIHNRMTTLSSLEKVN 320
   ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 201 TAKRMDHISNAVES---KONADYNTSLADIWGRALAYNFPSLNNGGICLTWSSIRD--- 254
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 321 TAQCPLEFTCLHVRDVSELMFADWVEESPYEIGMAKGTGMADPLFGSKFP-MGYVVK 379

```


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DR EMBL: U02967; AAA03447.1; -
DR InterPro: IPR000008; -
DR InterPro: IPR0000719; -
DR InterPro: IPR000061; -
DR InterPro: IPR001245; -
DR InterPro: IPR002219; -
DR InterPro: IPR002290; -
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00130; DAG-PE-bind; 2.
DR Pfam: PF00069; Kinase; 1.
DR Pfam: PF00433; Kinase; C; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR PRINTS: PR00360; C2DOMAIN.
DR PROSITE: PS00499; C2_DOMAIN_1; 1.
DR PROSITE: PS00049; DAG-PE_BIND_DOM_1; 2.
DR PROSITE: PS00081; DAG-PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding, transferase; Serine/threonine-protein kinase;
KW Phospholipid binding; Zinc; Repeat.
FT DOMAIN 28 77 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 93 142 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 164 251 C2 DOMAIN.
FT DOMAIN 325 583 PROTEIN KINASE.
FT NP_BIND 331 339 ATP (BY SIMILARITY).
FT BINDING 354 354 ATP (BY SIMILARITY).
FT ACT_SITE 449 449 BY SIMILARITY.
SQ SEQUENCE 658 AA: 74871 MW: 748527A49C835A2 CRC64;

Query Match 3.4%; Score 134; DB 1; Length 658;
Best Local Similarity 19.6%; Pred. No. 0.054;

Matches 103; Conservative 63; Mismatches 149; Indels 210; Gaps 27;

QY 43 DPEVLEFISTPD-----SRKTRHPNDINPVNNEFEFL--DPNOEVLLETTMDAN 95
DB 184 DPEVKL-KIIPQKRETKKRTKRTKINGSUNPTGESDFLEPTDRRLIVEVMD-R 240
QY 96 YNDEFILGATFTVSSM-----KVGEKKEVPFTINQVTEVLENSLEVCS 141
DB 241 ATNDEMGLAFSGISELMKAGVADWYKLLGQEEGEYVNPALAE--TESIDELTSNKKL 298
QY 142 PDARFEMALCDDOKTRQQRKEHRESMKLLGPKNSE-----GLMSARVPVAILGSG 196
DB 299 P-----MPEQEHVK-----PQNSNSMGKGVYRASDFNLSVLGKG 334
QY 197 GGFRAVVGSGVKALYESGIL-----DCA---TYVAGLSGSTVYMSLTLS--- 239
DB 335 SFGKVLAEKKGKDELKILKKDVIIDDVDECMTEKRVGLSKPFLALHLSFCFQ 394
QY 240 -----HPDPEPKPEEINELMKVSHNPLLLTPQKYKRYE-----SLW 280
DB 395 TMDRLFFVMEFVNGD-----LMFOIQKQKREPHAVFYAAEIAVGLF 438
QY 281 KKKSSGQPTFTDI-----EGMLIGETLIHNRMTTLLSKEXNTAQ 323
DB 439 YLHSGQ-VYIRPLKLDNVLDAEGHIKADPEM-----CKEHNNEG 479
QY 324 -----CPLFLCTLHVKPDVSELAFADWFEFSY--EIGMAKYGTMAPDLFGSKFFMG 376
DB 480 TTRTFCGTGTDY-----IAPEL-----VAYQPYGKAVDMMAFGVLLIETLALAGQPF 527

QY 377 VVKKEENPLFLMGWGSFSLFNRLVSGSOSRGS-TMEELENTTTHK---IYS 431
DB 528 -----DEDEL-----FQSIMHEVPSYKSMNSRSTYTM---CKGFLTKRGRILS 569
QY 432 NDSSDSDDESHE-----PKTENE 451
DB 570 GPTGEDIDREHGFERRIDWEKLANREIOPEFVPSVVRNPAEMND 614

RESULT 14

RP3A_RAT STANDARD; PRT; 684 AA.
ID RP3A_RAT
AC P47709;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE RABPHILIN-3A.
GN RPH3A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95033210; PubMed=7946335;
RA Li C., Takei K., Geppert M., Daniell L., Stenius K., Chapman E.R.,
RA Jahn R., de Camilli P., Suedhof T.C.;
RT "Synaptic targeting of rabphilin-3A, a synaptic vesicle
RT Ca2+/phospholipid-binding protein, depends on rab3A/3C".
RL Neuron 13:885-898(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 44-167 IN COMPLEX WITH RAB3A.
RX TISSUE=Brain;
RX MEDLINE=99148269; PubMed=10025402;
RA Ostermeier C., Brunger A.T.;
RT "Structural basis of Rab effector specificity: crystal structure of
RT the small G protein Rab3a complexed with the effector domain of
RT rabphilin-3A".
RL Cell 96:363-374(1999).
CC -1- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED WITH RAS-RELATED
CC PROTEIN RAB-3A IN SYNAPTIC VESICLE TRAFFIC AND/OR SYNAPTIC
CC VESICLE FUSION. COULD PLAY A ROLE IN NEUROTRANSMITTER RELEASE BY
CC REGULATING MEMBRANE FLOW IN THE NERVE TERMINAL.
CC -1- SUBUNIT: MONOMER.
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN BRAIN.
CC -1- SIMILARITY: CONTAINS 2 C2 DOMAINS.
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DR EMBL: U12571; AAA2662.1; -
DR PDB: 1ZBD; 12-APR-99.
DR InterPro: IPR000008; -
DR InterPro: IPR001565; -
DR InterPro: IPR001965; -
DR Pfam: PF00168; C2; 2.
DR Pfam: PF00628; PHD; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00399; SYNAPTOTAGMN.
DR PROSITE: PS00499; C2_DOMAIN_1; 2.
DR PROSITE: PS00004; C2_DOMAIN_2; 2.
KW Repeat; Synapse; Protein transport; 3D-structure.
FT DOMAIN 397 645 PHOSPHOLIPID BINDING (PROBABLE).
FT DOMAIN 557 645 C2 DOMAIN.
SQ SEQUENCE 684 AA: 75832 MW: 05838BC3C7A86444 CRC64;

[illegible]

Search completed: July 31, 2001, 16:33:29
Job time: 196 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 31, 2001, 16:29:13 ; Search time 19.33 Seconds
(without alignments)
2951.616 Million cell updates/sec

Title: US-09-250-083a-2

Sequence: 1 MSFIDPYGHIIIVHQYSHKF.....LSNVEARRRPNKFLSKPKA 749

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_68:***
2: PIR1:***
3: PIR2:***
4: PIR3:***
5: PIR4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3942	100.0	749	A39329	phospholipase A2 (
2	3763	95.5	749	B39898	cytosolic phosphol
3	3391	86.0	748	I50699	phospholipase A2 c
4	2791	70.8	741	B54508	cytosolic phosphol
5	494.5	12.5	541	T13162	lysophospholipase
6	221.5	5.6	612	S29318	PLB1 protein - yea
7	219.5	5.6	664	S53037	lysophospholipase
8	209.5	5.3	754	T18238	lysophospholipase
9	207.5	5.3	706	S53035	lysophospholipase
10	205.5	5.2	666	S66933	hypothetical prote
11	194.5	4.9	623	T40991	probable lysophosp
12	192.5	4.9	624	T38006	probable lysophosp
13	178.5	4.5	574	T51799	CUH1-like protein
14	172.5	4.4	510	T50526	CaLB protein - Ara
15	170.5	4.3	613	T38007	probable lysophosp
16	169	4.3	644	T37800	probable lysophosp
17	163.5	4.1	673	T50281	lysophospholipase
18	148.5	3.8	536	S62110	anthranilate phosph
19	140.5	3.6	972	T47922	alpha-toxin - Clos
20	140.5	3.6	2178	S55805	anthranilate phosph
21	138.5	3.5	773	T46010	anthranilate phosph
22	135.5	3.4	505	T04143	CUH1 protein - tom
23	134.5	3.4	776	C96554	unknown protein [i
24	129	3.3	1278	A47462	probable DNA-direc
25	128	3.2	681	TJX0338	rabphilin-3A - mou
26	128	3.2	684	T58166	rabphilin-3A - rat
27	128	3.2	1096	S62358	inositol 1,4,5-tri
28	126.5	3.2	2104	T38774	myosin-3 heavy cha
29	125	3.2	704	A48097	rabphilin-3A - bov

30	122.5	3.1	854	1	WMBP22	gene 12 protein -
31	122.5	3.1	1178	2	S54073	probable membrane
32	121.5	3.0	769	2	T49911	anthranilate phosph
33	121	3.1	675	2	T01234	probable anthranil
34	119	3.0	857	2	T04208	probable anthranil
35	119	3.0	2475	2	S35307	polyprotein pp220
36	118.5	3.0	592	2	T50516	Ca2+ dependent 11p
37	118.5	3.0	664	2	T24459	hypothetical prote
38	117.5	3.0	779	2	T01304	hypothetical prote
39	117.5	3.0	1173	2	T51440	alpha-mannosidase-
40	117.5	3.0	1299	2	T24299	hypothetical prote
41	116.5	3.0	1024	2	D81624	exodeoxyribonuclea
42	116.5	3.0	1216	2	A28821	1-phosphatidylinos
43	116.5	3.0	1777	2	T00490	nonstructural prot
44	116	2.9	504	2	A29410	cytochrome P450, g
45	115.5	2.9	1024	2	F86582	exodeoxyribonuclea

ALIGNMENTS

RESULT 1
A39329
Phospholipase A2 (EC 3.1.1.4), cytosolic - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
C:Accession: A39329; A39898; A54198; S68898
R:Sharp, J.D.; White, D.L.; Chou, X.G.; Goodson, T.; Gamboa, G.C.; McClure, D.; Burg
J. Biol. Chem. 266, 14850-14853, 1991
A:Title: Molecular cloning and expression of human Ca(2+)-sensitive cytosolic phospho
A:Reference number: A39329; MUID:91331987
A:Accession: A39329
A:Molecule type: mRNA
A:Residues: 1-749 <SHA>
A:Cross-references: GB:M68874; NID:g190003; PIDN:AAA60105.1; PID:g190004
A:Note: part of this sequence was confirmed by protein sequencing
R:Clark, J.D.; Lin, L.L.; Kriz, R.W.; Ramesha, C.S.; Sultzman, L.A.; Lin, A.Y.; Milon
Cell 65, 1043-1051, 1991
A:Title: A novel arachidonic acid-selective cytosolic PLA-2 contains a Ca(2+)-depende
A:Reference number: A39898; MUID:91256305
A:Accession: A39898
A:Molecule type: mRNA
A:Residues: 1-749 <CLA>
A:Cross-references: GB:M72393; NID:g190006; PIDN:AAB00789.1; PID:g190007
R:Li, B.; Copp, L.; Castelhamo, A.L.; Feng, R.; Stahl, M.; Yuan, Z.; Krantz, A.
Biochemistry 33, 8594-8603, 1994
A:Title: Inactivation of a cytosolic phospholipase A-2 by thiol-modifying reagents: c
A:Reference number: A54198; MUID:94304876
A:Accession: A54198
A:Molecule type: protein
A:Residues: 319-338, 'X', 340-345, 'X', 347-358 <LIA>
A:Note: modification of preferred modification site Cys-324 abolished enzymatic activ
R:Gordon, R.D.; Leighton, I.A.; Campbell, D.G.; Cohen, P.; Creaney, A.; Willton, D.C.;
Eur. J. Biochem. 238, 690-697, 1996
A:Title: Cloning and expression of cytosolic phospholipase A(2) (cPLA(2)) and a natur
results in an increase in specific activity.
A:Reference number: S68897; MUID:96300233
A:Accession: S68898
A:Molecule type: protein
A:Residues: 497-507 <GOR>
C:Comment: This cytosolic phospholipase A2 translocates to membrane vesicles in respo
C:Genetics:
A:Gene: GDB:PIA2G4A; PIA2G4
A:Cross-references: GDB:134687; OMIM:600522
A:Map position: 1q25-1q25
C:Superfamily: cytosolic phospholipase A2
C:Keywords: calcium; carboxylic ester hydrolase; cytosol; inflammation; phosphoprotei
F:505/inding site: phosphate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 3942; DB 1; Length 749;
Best Local Similarity 100.0%; Pred. No. 9, 1e-280;

Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFIDYQHIIIVEHOXSHKFTVVVLRATKVTKGAFGMDLTPDPYVELFISTTPDSKRT 60
 Db 1 MSFIDYQHIIIVEHOXSHKFTVVVLRATKVTKGAFGMDLTPDPYVELFISTTPDSKRT 60

QY 61 RHEINDINPVWNETFEFILLDPNOENVLEITLMDANYVMDLTGATFTVSMKVGKREY 120
 Db 61 RHEINDINPVWNETFEFILLDPNOENVLEITLMDANYVMDLTGATFTVSMKVGKREY 120

QY 121 PFIENOVTEVMELEMSLEVCSCPLRFSMALCDEKTFRQQRKEHIRESMKLLGPKNSG 180
 Db 121 PFIENOVTEVMELEMSLEVCSCPLRFSMALCDEKTFRQQRKEHIRESMKLLGPKNSG 180

QY 181 LHSARDVPVVAIIIGSGGFRAMVFGSGVMKALYESGILDCAITYAGLSGTWMTLYSH 240
 Db 181 LHSARDVPVVAIIIGSGGFRAMVFGSGVMKALYESGILDCAITYAGLSGTWMTLYSH 240

QY 241 PDFPEKGPEEINELMKNSHNPDLTLTPQVKRYVESLTKKSSGQPVTFDIFGMLIG 300
 Db 241 PDFPEKGPEEINELMKNSHNPDLTLTPQVKRYVESLTKKSSGQPVTFDIFGMLIG 300

QY 301 ETLIHRMNTTSLSEKRYNTAOCPLPFTCLHVKRPDVSLEMFADWVEFSPEIGMAKYG 360
 Db 301 ETLIHRMNTTSLSEKRYNTAOCPLPFTCLHVKRPDVSLEMFADWVEFSPEIGMAKYG 360

QY 361 TFMAPDLFGSKFPMGTIVVKKYEENPLHFLMGVGSASFILFNVLGVSQSOGSTMEBE 420
 Db 361 TFMAPDLFGSKFPMGTIVVKKYEENPLHFLMGVGSASFILFNVLGVSQSOGSTMEBE 420

QY 421 LENITTKHIVSNDSSDDESHKPTENEDAGSDYQSDNOASWIRHIMATVSDSALFN 480
 Db 421 LENITTKHIVSNDSSDDESHKPTENEDAGSDYQSDNOASWIRHIMATVSDSALFN 480

QY 481 TREGRAGKVNEMFLGINTSYPLSPDPAOTQDSFDDDELDAVAADPDEFERIEPLDY 540
 Db 481 TREGRAGKVNEMFLGINTSYPLSPDPAOTQDSFDDDELDAVAADPDEFERIEPLDY 540

QY 541 KSKKIHVDSGLTFNLPLYLLRPQGVDLISFDSARPSSDSSPPFKELLAEKAKNM 600
 Db 541 KSKKIHVDSGLTFNLPLYLLRPQGVDLISFDSARPSSDSSPPFKELLAEKAKNM 600

QY 601 KLPFPKIDPVFREGIACGYFKPKNPDMKDCPTIIHFVLANINFRKXKAPGVRETE 660
 Db 601 KLPFPKIDPVFREGIACGYFKPKNPDMKDCPTIIHFVLANINFRKXKAPGVRETE 660

QY 661 EEKEIADFIDDPESPSTFNFQYRNAQAFKRLHDLMHFNTLNNIDVKEAMVESTIYRR 720
 Db 661 EEKEIADFIDDPESPSTFNFQYRNAQAFKRLHDLMHFNTLNNIDVKEAMVESTIYRR 720

QY 721 QNPSRCSVSLSNVEARFRFNKEFLSKPKA 749
 Db 721 QNPSRCSVSLSNVEARFRFNKEFLSKPKA 749

RESULT 2

B39898
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: B39898
 R:Clark, J.D.; Lin, L.L.; Kriz, R.W.; Ramesha, C.S.; Sultzman, L.A.; Lin, A.Y.; Milona, Cell 65, 1043-1051, 1991
 A:Title: A novel arachidonic acid-selective cytosolic PLA-2 contains a Ca(2+)-dependent
 A:Reference number: A39898; MUID:91256305
 A:Accession: B39898
 A:Molecule type: mRNA
 A:Residues: 1-749 <CLAA>
 A:Cross-references: GB:M72394
 C:Comment: This cytosolic phospholipase A2 translocates to membrane vesicles in response
 C:Superfamily: cytosolic phospholipase A2
 C:Keywords: calcium, carboxylic ester hydrolase; cytosol; inflammation

Query Match 95.5%; Score 3763; DB 1; Length 749;
 Best local similarity 94.9%; Pred. No. 1,1e-266;
 Matches 709; Conservative 24; Mismatches 14; Indels 0; Gaps 0;

QY 1 MSFIDYQHIIIVEHOXSHKFTVVVLRATKVTKGAFGMDLTPDPYVELFISTTPDSKRT 60
 Db 1 MSFIDYQHIIIVEHOXSHKFTVVVLRATKVTKGAFGMDLTPDPYVELFISTTPDSKRT 60

QY 61 RHEINDINPVWNETFEFILLDPNOENVLEITLMDANYVMDLTGATFTVSMKVGKREY 120
 Db 61 RHEINDINPVWNETFEFILLDPNOENVLEITLMDANYVMDLTGATFTVSMKVGKREY 120

QY 121 PFIENOVTEVMELEMSLEVCSCPLRFSMALCDEKTFRQQRKEHIRESMKLLGPKNSG 180
 Db 121 PFIENOVTEVMELEMSLEVCSCPLRFSMALCDEKTFRQQRKEHIRESMKLLGPKNSG 180

QY 181 LHSARDVPVVAIIIGSGGFRAMVFGSGVMKALYESGILDCAITYAGLSGTWMTLYSH 240
 Db 181 LHSARDVPVVAIIIGSGGFRAMVFGSGVMKALYESGILDCAITYAGLSGTWMTLYSH 240

QY 241 PDFPEKGPEEINELMKNSHNPDLTLTPQVKRYVESLTKKSSGQPVTFDIFGMLIG 300
 Db 241 PDFPEKGPEEINELMKNSHNPDLTLTPQVKRYVESLTKKSSGQPVTFDIFGMLIG 300

QY 301 ETLIHRMNTTSLSEKRYNTAOCPLPFTCLHVKRPDVSLEMFADWVEFSPEIGMAKYG 360
 Db 301 ETLIHRMNTTSLSEKRYNTAOCPLPFTCLHVKRPDVSLEMFADWVEFSPEIGMAKYG 360

QY 361 TFMAPDLFGSKFPMGTIVVKKYEENPLHFLMGVGSASFILFNVLGVSQSOGSTMEBE 420
 Db 361 TFMAPDLFGSKFPMGTIVVKKYEENPLHFLMGVGSASFILFNVLGVSQSOGSTMEBE 420

QY 421 LENITTKHIVSNDSSDDESHKPTENEDAGSDYQSDNOASWIRHIMATVSDSALFN 480
 Db 421 LENITTKHIVSNDSSDDESHKPTENEDAGSDYQSDNOASWIRHIMATVSDSALFN 480

QY 481 TREGRAGKVNEMFLGINTSYPLSPDPAOTQDSFDDDELDAVAADPDEFERIEPLDY 540
 Db 481 TREGRAGKVNEMFLGINTSYPLSPDPAOTQDSFDDDELDAVAADPDEFERIEPLDY 540

QY 541 KSKKIHVDSGLTFNLPLYLLRPQGVDLISFDSARPSSDSSPPFKELLAEKAKNM 600
 Db 541 KSKKIHVDSGLTFNLPLYLLRPQGVDLISFDSARPSSDSSPPFKELLAEKAKNM 600

QY 601 KLPFPKIDPVFREGIACGYFKPKNPDMKDCPTIIHFVLANINFRKXKAPGVRETE 660
 Db 601 KLPFPKIDPVFREGIACGYFKPKNPDMKDCPTIIHFVLANINFRKXKAPGVRETE 660

QY 661 EEKEIADFIDDPESPSTFNFQYRNAQAFKRLHDLMHFNTLNNIDVKEAMVESTIYRR 720
 Db 661 EEKEIADFIDDPESPSTFNFQYRNAQAFKRLHDLMHFNTLNNIDVKEAMVESTIYRR 720

QY 721 QNPSRCSVSLSNVEARFRFNKEFLSKPKA 747
 Db 721 QNPSRCSVSLSNVEARFRFNKEFLSKPKA 747

RESULT 3

I50699
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: I50699
 R:Nalefski, E.A.; Sultzman, L.A.; Martin, D.M.; Kriz, R.W.; Towler, P.S.; Knopf, J.L. J. Biol. Chem. 269, 18239-18249, 1994
 A:Title: Delineation of two functionally distinct domains of cytosolic phospholipase
 A:Reference number: A54908; MUID:94299545
 A:Accession: I50699
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-748 <NAA>
 A:Cross-references: EMBL:U010329; NID:g508624; PIDN:AAA53228.1; PID:g508625

C:Superfamily: cytosolic phospholipase A2
C:Keywords: cytosol

Query Match 86.0%; Score 3391; DB 1; Length 748;
Best Local Similarity 83.9%; Pred. No. 1,6e-239;
Matches 625; Conservative 64; Mismatches 56; Indels 0; Gaps 0;

QY 1 MSFIDPQHIIIVEHSHKFTVVVLRATKYKGAFGMDLTPDPYVELFISTPDSRRKT 60
DB 1 MSFIDPQHIIIVEHSHKFTVVVLRATKYKGAFGMDLTPDPYVELFISTPDSRRKT 60
QY 61 RHFNDINPWNNEFEFLDPNÖENVLETIMADNYVDELTGATFTVSSMKYGEKEV 120
DB 61 RHFNDINPWNNEFEFLDPNÖENVLETIMADNYVDELTGATFTVSSMKYGEKEV 120
QY 121 PFIRNOVTEWYLEMSLEVCSPDLRFMSALCDDEKTRQOKREHIRESKMLLPKNSG 180
DB 121 QLTNNVTENTLELSLEVCSTDLRFMSALCDDEKTRQOKREHIRESKMLLPKNSG 180
QY 181 LHSADVPVVAIIISGGGFRAMVGFSGVMKALYESGILDCATYVAGISGTWYSTLYSH 240
DB 181 LHSADVPVVAIIISGGGFRAMVGFSGVMKALYESGILDCATYVAGISGTWYSTLYSH 240
QY 241 PDPEKPEEELNEELKKNVSNPLLLTPOKVRYVESLKKKSSGQPVTFDIFGMLIG 300
DB 241 PDPEKPEEELNEELKKNVSNPLLLTPOKVRYVESLKKKSSGQPVTFDIFGMLIG 300
QY 301 ETLHNMMNTLSSIKKRVNTAOCPLPFTCLHYKPDVSELMFADWVEFSYEIGMAKYG 360
DB 301 ETLHNMMNTLSSIKKRVNTAOCPLPFTCLHYKPDVSELMFADWVEFSYEIGMAKYG 360
QY 361 TFAPADLFSGKFEGTVYKKEENPLHFLMGVGSASFILFNRYLGVSQSGSTMEEE 420
DB 361 TFAPADLFSGKFEGTVYKKEENPLHFLMGVGSASFILFNRYLGVSQSGSTMEEE 420
QY 421 LENTTHIYVNDSDSDSHPEKGTENEDAGSDYOSDNOASWIRHIMAVSDALEN 480
DB 421 LENTTHIYVNDSDSDSHPEKGTENEDAGSDYOSDNOASWIRHIMAVSDALEN 480
QY 481 TREGRACKVHFMGLNLTSTPLSDFAOTDSFDDDELDAVADDEERIEPLDY 540
DB 481 TREGRACKVHFMGLNLTSTPLSDFAOTDSFDDDELDAVADDEERIEPLDY 540
QY 541 KSKRIHVDSGLTFENLPYLLRPQRCVDLIISFDSARPDSPPFEKELLAEKMAKN 600
DB 541 KSKRIHVDSGLTFENLPYLLRPQRCVDLIISFDSARPDSPPFEKELLAEKMAKN 600
QY 601 KLPPKIDPVPFDEGLKECYVFKPKNDMEKDCPTIIHFVLANINFRKYKAPGVPRETE 660
DB 601 KLPPKIDPVPFDEGLKECYVFKPKNDMEKDCPTIIHFVLANINFRKYKAPGVPRETE 660
QY 661 EEKRIADFIDDPESPFPNFPOYRNOAFKRLDLMHFNLTNIDVYKEMAVESIEYR 720
DB 661 EEKRIADFIDDPESPFPNFPOYRNOAFKRLDLMHFNLTNIDVYKEMAVESIEYR 720
QY 721 QNPSRCSVSLNVEARFPFNKELS 745
DB 721 QNPSRCSVSLNVEARFPFNKELS 745

RESULT 4

B54908
Phospholipase A2 cytosolic - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 07-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 31-Oct-1997
C:Accession: B54908
R:Meleleski, E.A.; Sultzman, L.A.; Martin, D.M.; Kriz, R.W.; Towler, P.S.; Knopf, J.L.;
J. Biol. Chem. 269, 18239-18249, 1994
A:Title: Delineation of two functionally distinct domains of cytosolic phospholipase A2;
A:Accession: B54908
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-741 <NML>
A:Cross-references: EMBL:U0329
C:Superfamily: cytosolic phospholipase A2

Query Match 70.8%; Score 2791; DB 2; Length 741;
Best Local Similarity 72.7%; Pred. No. 1.1e-195;
Matches 537; Conservative 81; Mismatches 111; Indels 10; Gaps 7;

QY 9 HIIEHSHKFTVVVLRATKYKGAFGMDLTPDPYVELFISTPDSRRKRRHFNNDIN 68
DB 3 NIIEHSHKFTVVVLRATKYKGAFGMDLTPDPYVELFISTPDSRRKRRHFNNDIN 62
QY 69 PVNNEFEFLDPNÖENVLETIMADNYVDELTGATFTVSSMKYGEKEVPIFNQV 128
DB 69 PVNNEFEFLDPNÖENVLETIMADNYVDELTGATFTVSSMKYGEKEVPIFNQV 122
QY 129 EMVLEMSLEVCSPDLRFMSALCDDEKTRQOKREHIRESKMLLPKNSGHLHA-RDV 187
DB 123 KVFLLILEVCASDTDLRFMSALCDDEKTRQOKREHIRESKMLLPKNSGHLHA-RDV 182
QY 188 PVVAIIISGGGFRAMVGFSGVMKALYESGILDCATYVAGISGTWYSTLYSHDPEPKG 247
DB 183 PVVAIIISGGGFRAMVGFSGVMKALYESGILDCATYVAGISGTWYSTLYSHDPEPKG 242
QY 248 PEEINEELKKNVSNPLLLTPOKVRYVESLKKKSSGQPVTFDIFGMLIGETLHNH 307
DB 243 PGDINKELKKNVSNPLLLTPOKVRYVESLKKKSSGQPVTFDIFGMLIGETLHNH 302
QY 303 NMLTSLIKERKRVNTAOCPLPFTCLHYKPDVSELMFADWVEFSYEIGMAKYGTFMSPGL 367
DB 303 NMLTSLIKERKRVNTAOCPLPFTCLHYKPDVSELMFADWVEFSYEIGMAKYGTFMSPGL 362
QY 368 FGSKFEGTVYKKEENPLHFLMGVGSASFILFNRYLGVSQSGSTMEEELENTTK 427
DB 363 FGSKFEGTVYKKEENPLHFLMGVGSASFILFNRYLGVSQSGSTMEEELENTTK 421
QY 428 HIVNDSDSDESHPEKGTENEDAGSDYOSDNOASWIRHIMAVSDALENREGAG 487
DB 422 HIVNDSDSDESHPEKGTENEDAGSDYOSDNOASWIRHIMAVSDALENREGAG 480
QY 488 KVHFMGLNLTSTPLSDFAOTDSFDDDELDAVADDEERIEPLDYVSKKIHV 547
DB 481 KVHFMGLNLTSTPLSDFAOTDSFDDDELDAVADDEERIEPLDYVSKKIHV 538
QY 548 VDSGLTFENLPYLLRPQRCVDLIISFDSARPDSPPFEKELLAEKMAKNLPKPI 607
DB 539 VDSGLTFENLPYLLRPQRCVDLIISFDSARPDSPPFEKELLAEKMAKNLPKPI 598
QY 608 DPVYFDRGLKECYVFKPKNDMEKDCPTIIHFVLANINFRKYKAPGVPRETEKEETAD 667
DB 599 DSKYFDRGLKECYVFKPKNDMEKDCPTIIHFVLANINFRKYKAPGVPRETEKEETAD 656
QY 668 FDIDDPESPFPNFPOYRNOAFKRLDLMHFNLTNIDVYKEMAVESIEYRONPSRCS 727
DB 657 FDIDDPESPFPNFPOYRNOAFKRLDLMHFNLTNIDVYKEMAVESIEYRONPSRCS 716
QY 728 VSLNVEARFPFNKELS 746
DB 717 VSLNVEARFPFNKELS 732

RESULT 5

T13162
Cytosolic phospholipase A2 gamma - human
N:Alternate names: protein DKFZp586C0423.1
C:Species: Homo sapiens (man)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: T13162; T08799
R:Pickard, R.T.; Striffler, B.A.; Kramer, R.M.; Sharp, J.D.
J. Biol. Chem. 274, 8823-8831, 1999
A:Title: Molecular cloning of two new human paralogs of 85-kDa cytosolic phospholipase

A:Reference number: 217618; MUID:99185108
 A:Accession: T13162
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-541 <PIC>
 A:Cross-references: EMBL:AF065214; NID:93811344; PID:93811345; PIDN:AAC78835.1
 R:Ansgorge, W.; Winkler, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, May 1999
 A:Reference number: 216472
 A:Accession: T08799
 A:Molecule type: mRNA
 A:Residues: 443-541 <ANS>
 A:Cross-references: EMBL:AL050193
 A:Experimental source: adult uterus; clone DKFZp586C0423
 C:Genetics:
 A:Gene: cPLA2 gamma
 A:Map position: 19
 A:Note: DKFZp586C0423.1

Query Match 12.5%; Score 494.5; DB 2; Length 541;
 Best Local Similarity 26.8%; Pred. No. 3,6e-28;
 Matches 199; Conservative 88; Mismatches 190; Indels 129; Gaps 20;

135 SLEVSCPDLFMSALCDQEKTRQQRKEHIRESMKKLLGPKNSEGLHSARDVVAALIG 194
 3 SSVSTIIPGLQ-----KEEKAVERRRRLHVKALKKL-----RIEADAPVVAVLG 48
 195 SGGGFAMGCFSGVMKALYESGILDCATYVAGSGSTWYWTIXSHDPPEKPEELINEE 254
 49 SGGGLAHNLACGLVLEMEQGLDVAITYLAGVSGSTWALISLYTN-----DDMALFA 103
 255 LMKVSHNPILLTLPQKVKRYVESLMKKSSGQPV-----TFDIMGILGETLIH 305
 104 DLKH-----RFTQENDLAKSLQKTOAASENYSUTDFAYAVYISKQTR 148
 306 NRMNTLSIKERKYNATQCPRLPTCL--HKPDVSELMEFAD--WVESPYEIGMAYGTF 362
 149 ELPEHSLNKKKRYVEEGTLPRPIFAIDNDLQPSMOEARAPETWFTPHHAGFPALGAF 208
 363 MAPDLGSKPFMTQVYKKYEENLHLMGVWGSAPSTLFRVLYGSGSGSGST----- 416
 209 VSTTHGSKFKKRLVTRHERDLTFLRLGLWSAL-----GNTVEYIREY 252
 417 MEELENITTKH-----VSNDSS-----SDDESHPEKTEREDAGSYQSD 459
 253 IFQQLNLTGLKMRRAVNAKSTIGHLIFARLRLQESSGGEHPP-----EDGG-----GE 304
 460 NQASWTHRM-----MALVSDSALFNTREGRAKVHNFMLGLNLTSTPLSLDEATOD 514
 305 PEHTWLTLEMLNTRTSLEKQEQHEDPE--RKGSLSNLM-----DEVKKT 348
 515 SFDDDELDAVADPDEER--IYEPIDVSKKTHVYDSGLTFLPPLIIRPGRVDLI 572
 349 GICASKWEGTTHNPLFKHGIDKIMSSRKHLALVDAGLAINTPPPLVLPPIREHLLI 408
 573 SFDFSARPSDSPFKELLAEKMAKNKLPFKPIDPYVD--REGLECYVFKPKPNPM 630
 409 SDFPSA-----GDFETIARTTYDCRHKIPFQVEAEELDMASKAPACIILKGETG-- 461
 631 EKDCPTIHFVLANIN 646
 462 ----PVVMHPELFENID 473

RESULT 6
 S29318
 lysophospholipase (EC 3.1.1.5) precursor [validated] - Penicillium notatum (fragment)
 C:Species: Penicillium notatum
 C:Date: 10-Mar-1994 #sequence,revision 10-Mar-1994 #text_change 19-Jan-2001
 C:Accession: S29318; S39881; S22045
 R:Masuda, N.; Kitamura, N.; Saito, K.
 Eur. J. Biochem. 202, 783-787, 1991

A:Title: Primary structure of protein moiety of Penicillium notatum phospholipase B d
 A:Reference number: S29318; MUID:92111525
 A:Accession: S29318
 A:Molecule type: mRNA
 A:Residues: 1-612 <MAL>
 A:Cross-references: EMBL:X60348; NID:93183; PIDN:CAA2906.1; PID:93184
 A:Accession: S39881
 A:Molecule type: protein
 A:Residues: 10-20;185-199 <MA2>
 C:Superfamily: yeast lysophospholipase
 C:Keywords: carboxylic ester hydrolase; glycoprotein
 F:1-9/Domain: signal sequence (fragment) #status predicted <SIG>
 F:10-612/Product: lysophospholipase #status experimental <MAT>
 F:41,81,116,223,267,306,335,427,440,446,477,498,526,532,567,571/Binding site: carboxy

Query Match 5.6%; Score 221.5; DB 2; Length 612;
 Best Local Similarity 22.6%; Pred. No. 3.8e-08;
 Matches 112; Conservative 78; Mismatches 145; Indels 161; Gaps 24;

140 SCPDLRFSMALDQEKTRQQRKEHIRESMKKLLG-----PKNSRGLHSARD 186
 28 SRFVTSAAKLSTNYSWLEVRGKTLALDKDFGHVKKGDYDGYALDKHS---GNSS 84
 187 VPVVAITLGGGFRAMVGFSGVKAL-----YESGILDCATYVAGSGSTWYMS 235
 85 LPIGILAVSGGGRALMNGAVKAFDSRDNATATGHLGGLQASATYISGLSGSWLLG 144
 236 TLVSHDFPE-----KPEELNEELMKVSHNPILLTLPQVKRY 275
 145 SIYIN-NFTTVDKLQTHAGSVWQFGNSIIEGPDAGIOLLDSAGY-----YKDL 193
 276 VESLTKKSSGQGVPTDFGMLIGETLI--HNRNNTLSLKE--KYNTAQCPPLPT 330
 194 ADVAVDKKRAKGFPTITLDIGRALSYQMRNASNGSLTYWSSIADPPEQDDYPRPFV 253
 331 CLAVKPDVSELMF--ADVVESPYEIGMAYGTFMAPDLFSGKPFMGVYVKKYENPLH 387
 254 ADGRNP--GELVIGNSIYVEFNPMW--FCTF-DPTIFG--FV-----PLE 292
 388 FLMGWGSAPSTLFRNVLGVSGSGSTMEELNITTKHIVSNDSSSDDESHPEKKT 447
 293 YL-----GSKFEGSLP-----SNMSCIRGSDS----- 315
 448 ENEDAGSDYQSDNQASWTHRMIALVSDSALFNTREGRAKVHNFMLGLNLTSTPL 507
 316 ----AG-----FVIGTSSLEN-----QFLQTN-TTSLP-SFI 343
 508 SDFATQDSFDD--ELDAVADPDEPERIYEPDL--VSKKTHVYDSGLT-FNLPPPLI 562
 344 KDFENGILFDLDKSDIASYDPNPYKYNHSSPYAAQKLDVVDVGDGQNVPLHPLI 403
 563 RPRQGVDLIISDFSA 578
 404 QPERHVDVIFAVDSSA 419

RESULT 7
 S53037
 PLB1 protein - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YH8270.10c; protein YKR008c
 C:Species: Saccharomyces cerevisiae
 C:Date: 08-Jul-1995 #sequence,revision 01-Sep-1995 #text_change 18-Jun-1999
 C:Accession: S53037; A53647
 R:Devlin, K.; Churcher, C.M.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53037
 A:Molecule type: DNA
 A:Residues: 1-664 <DEV>
 A:Cross-references: EMBL:Z48613; NID:9728645; PIDN:CAA88523.1; PID:9728655; MIPS:YKR0
 A:Experimental source: strain AB972
 R:Lee, K.S.; Patton, J.L.; Fido, M.; Hines, L.K.; Kohlwein, S.D.; Paltauf, F.; Henry,


```

QY 19 KFTVVVLRATKVGAFGDMIDTPDPYVELFISTPDSRRKTRHNNINPVNTEFEFI 78
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 272 KLDVAVVQAKDL---ANDDMIGKSPVAIVFIRLPDRTKTKTISNLPNHNHFEEFI 328
QY 79 LDPNOENVLEITLMDANY-MDETLGATFTVSSMKVGEKKEVPEIFNOVTEVLEMSLEV 134
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 329 VEDVSTOHLTVRFVDEGVSSQLGAAOVPLNELVPGKVDI--WLKLVLDLEIORDTK 386
QY 135 ---SLEVSCSP-----DLRFMALCDQEKTFQOQKEHIRESMKKILGKNSKSE- 179
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 387 NRGQLELLCYCPGKEGGLKNFPNPYSLTIL--EKVLKPEESDSDATMKKLVTSKKKDV 444
QY 180 ---GLHS-----ARDPVVAIISGCGFRAMVFGSGVKKALYESGILDCATYVAGLSGT 231
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 445 IVRGLSTTVVAABEDLPVADPMGRKDAF-----VITLKKSTKSKTRVYDPDSLNPV 496
QY 232 WYMSTLYSHPPPEPEKPEEINEELKNVSHNPLLL-----LTPQKVRVYESLMKKRS 284
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 497 WNOQF-----DF-----VEDALHDLTLEVDHDKFKDKIGRIVMTLTRYVWL 540
QY 285 SGQPTFTDIFGMLGETLIH 305
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 541 EGEFOEFELDGANSGLCVH 561

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RESULT 14

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T50526
Calc protein - Arabidopsis thaliana
N:Alternate names: protein T27115_140
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: T50526
R:Choiame, N.; Robert, C.; Brottier, P.; Wincker, P.; Catolico, L.; Arliguenave, F.; Se
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25102
A:Accession: T50526
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-510 <CHO>
A:Cross-references: EMBL:AL358732
A:Experimental source: cultivar Columbia; BAC clone T27115
C:Genetics:
A:Map position: 3
A:Insertions: 352/3; 86/3; 127/1; 166/3; 199/3; 226/3; 255/2; 330/3; 385/3
A:Note: T27115_140

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Query Match 4.48; Score 172.5; DB 2; Length 510;
Best Local Similarity 28.08; Pred. No. 0.00011;
Matches 58; Conservative 37; Mismatches 89; Indels 23; Gaps 8;

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QY 19 KFTVVVLRATKVGAFGDMIDTPDPYVELFISTPDSRRKTRHNNINPVNTEFEFI 78
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 264 KLIYVAVATNKN---KELIGKSDPAVITYI--RPVKYTKALENNLPVWDTEFELI 318
QY 79 LDPNOENVLEITLMDANY-MDETLGATFTVSSMKVGEKKEVPEIFNOVTEVLEMSLEV 138
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 319 AEDRQGLTVEVFPDKVGDGRGLVGLKLPLSLSLAGVTKEI-----ELNLLSLSDT 370
QY 139 CSCPDL--RFSMALCDQEKTFQOQKEHIRESMKKILGP---KNSELSHARDVPVAI 192
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 371 LKVKDKKRGSTTLKLVHYHEFNKEQMAALDEDEKIMEERRKLEAGVIGTMD--AVGM 428
QY 193 LGSQ-GGFRAMVGS-GVMKALYESGI 217
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 429 VSGGLGAGVGMVGTGIGVGLVSGV 455

```

RESULT 15

```

T38007
Probable lysophospholipase (EC 3.1.1.5) precursor SPAC1A6.04c [similarity] - fission yea
C:Species: Schizosaccharomyces pombe

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```

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-Jan-2001
C:Accession: T38007; T43005
R:Churcher, C.M.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21761
A:Accession: T38007
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-613 <CHD>
A:Cross-references: EMBL:Z29256; NID:g2414586; PIDN:CA16354.1; PID:g2414589; GSPDB:G
A:Experimental source: strain 972h; cosmid c1A6
R:Yoshioaka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722
A:Accession: T43005
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 338-613 <YOS>
A:Cross-references: EMBL:D89204; NID:g1749615; PIDN:BA13865.1; PID:g1749616
A:Experimental source: strain PR745
C:Genetics:
A:Gene: SPDB:SPAC1A6.04c
A:Map position: 1
A:Superfamily: yeast lysophospholipase
C:Keywords: carboxylic ester hydrolase

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Query Match 4.38; Score 170.5; DB 2; Length 613;
Best Local Similarity 21.98; Pred. No. 0.0002;
Matches 104; Conservative 74; Mismatches 186; Indels 111; Gaps 23;

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QY 154 EKTFRQQRKEHIRESMKKILGPKNSEGLH---SARDPVVAIISGCGFRAMVFGSGVM 209
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 74 ESEYISTSTITNTRAMKFLNANLPGLNADTLGSEBPSGIALSGGLAAMTIGSAL 133
QY 210 KAL-----YESGILDCATYVAGLSGTWYM-----STL-----YSHDPPE 245
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 134 SAMDARHDNHTVLGCLQASDYLVGTDSAMTVGIALNPNSTINDFSKLMAFNPLMYR 193
QY 246 KQPEEINEELKNVSHNPLLLTPQKVRVYESLMKKKSGQPTFTDIFGMLGETLI- 303
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 194 KSAIVFNHFTYSSI-----MNEVAEKNAGFNISLSDYWGKRVISRTLGD 237
QY 304 -IHNRMNTLSL--KEKVNTAOCPLPL--FTCLHYKPDVSELMFADWVEFSPEIGMAK 358
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 238 TTYGPNVSLSSITSQDEYRYRANPPYPIITFATQNYGDISNVN--TFEEASPNVFGTFD 296
QY 359 YG--TEMAPDLGSKF---FMGTVKKYEENPLHFLMGVGSNFSITLENRVL-GVSGS 410
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 297 HGINSFIPTFYIGTLLNNGASSNGSCVINYDN--FGFMWG---ASTYFNKIMRNFNDS 350
QY 411 QSRGSTMEELENTTKTIIVNSDSDSDSHPEPKGTEN--EDAGSDVQSDQAQMIHMI 469
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 351 STKNG-----RIIQQLKGNFSENGQIISIPPEFGVSNANSDAANN----- 393
QY 470 MALVSDALFNTREGKAGKVNFMGLNLTNTSYPLSLDEPATDPSFDDDLDAVADPD 529
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 394 --LGSSSSL-----NLVDTFLGKEI---PLMPL---LQKGRVDYI--VAVDNGD 434
QY 530 EPERY---EPLDVSKKIHVVDGLTFNLPLPLLPORGVDLLISFDSARP 580
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 435 DSEWLMPNGSLVQTYERYVAQAAGNTNVKGFYVPSQGS---FVSLHENDRP 485

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Search completed: July 31, 2001, 16:32:15
Job time: 182 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compgen Ltd.

OM protein - protein search, using sw model

Run on: July 31, 2001, 16:29:13 ; Search time 13.89 Seconds
(without alignments)
1110.307 Million cell updates/sec

Title: US-09-250-083A-2

Perfect score: 3942
Sequence: 1 MSFIDPYQHIIIVEHQYSHKF.....LSNVEARRFFNKELSRPKA 749

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3942	100.0	749	1	US-08-046-508-2
2	724	18.4	913	3	US-08-827-208-3
3	724	18.4	913	4	US-09-500-358-3
4	724	18.4	913	4	US-09-498-809-3
5	499.5	12.7	541	3	US-08-890-615-2
6	494.5	12.5	541	3	US-09-045-185-2
7	232.5	5.9	649	3	US-09-295-186-18
8	221.5	5.6	612	3	US-09-295-186-16
9	219.5	5.6	664	3	US-09-295-186-17
10	201.5	5.1	573	3	US-09-295-186-11
11	200.5	5.1	552	3	US-09-295-186-11
12	112	2.8	140	2	US-08-609-049A-16
13	108	2.7	897	1	US-08-095-737-4
14	108	2.7	897	1	US-08-480-145-4
15	108	2.7	897	2	US-08-477-389-4
16	107	2.7	688	1	US-08-221-817-19
17	107	2.7	688	1	US-08-454-439-19
18	107	2.7	688	5	PCT-US94-10487-19
19	103.5	2.6	808	1	US-08-471-251A-2
20	103	2.6	896	1	US-08-095-737-2
21	103	2.6	896	1	US-08-480-145-2
22	103	2.6	896	2	US-08-477-389-2
23	103	2.6	3418	2	US-08-639-501-2
24	103	2.6	3418	3	US-09-044-946-2
25	103	2.6	3418	3	US-08-755-587-44
26	103	2.6	3418	3	US-09-044-908-2
27	102	2.6	3418	2	US-08-603-753D-4

28	102	2.6	3418	4	US-09-099-753-4	Sequence 4, App11
29	102	2.6	3418	4	US-08-986-106-4	Sequence 4, App11
30	101.5	2.6	854	2	US-09-070-060-4	Sequence 4, App11
31	101.5	2.6	854	3	US-09-357-746-4	Sequence 4, App11
32	101	2.6	2938	5	PCT-US94-00198-3	Sequence 3, App11
33	100.5	2.5	873	3	US-09-187-331-6	Sequence 6, App11
34	100.5	2.5	904	6	5244792-4	Patent No. 5244792
35	100.5	2.5	911	3	US-09-356-952-6	Sequence 6, App11
36	100.5	2.5	925	2	US-08-392-946-1	Sequence 1, App11
37	100.5	2.5	925	2	US-08-504-169-1	Sequence 1, App11
38	100.5	2.5	925	5	PCT-US94-14893-1	Sequence 1, App11
39	100	2.5	984	1	US-08-242-932-2	Sequence 2, App11
40	100	2.5	984	1	US-08-714-481-2	Sequence 2, App11
41	100	2.5	984	5	5266464-2	Sequence 2, App11
42	99.5	2.5	671	6	5266464-2	Patent No. 5266464
43	97	2.5	2366	1	US-08-480-604A-10	Sequence 10, App11
44	97	2.5	2366	2	US-08-405-496A-10	Sequence 10, App11
45	96.5	2.4	904	4	US-08-632-537-1	Sequence 1, App11

ALIGNMENTS

RESULT 1
US-08-046-508-2
; Sequence 2, Application US/08046508
; Patent No. 5328842
; GENERAL INFORMATION:
; APPLICANT: Chlou et al.
; TITLE OF INVENTION: COMPOUNDS, VECTORS AND METHODS FOR
; TITLE OF INVENTION: EXPRESSING HUMAN CYTOSOLIC PHOSPHOLIPASE A2
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Patent Division/RSW
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,508
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph A. Jones
; REGISTRATION NUMBER: 26,472
; REFERENCE/DOCKET NUMBER: X-8477
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-5183
; TELEFAX: 317-276-1294
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 749 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-046-508-2

Query Match 100.0%; Score 3942; DB 1; Length 749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSFIDPYQHIIIVEHQYSHKFTVVVLRATKYTKGAFGMDLTPPYVELFISTPDSRKRT 60
|||||
DB 1 MSFIDPYQHIIIVEHQYSHKFTVVVLRATKYTKGAFGMDLTPPYVELFISTPDSRKRT 60
OY 61 RHFNNIDINPYWNETFEFILDPOENVALETTLMADANYVMDTGTATFTVYSKMGKEKEY 120

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Db 61 RHFNNDINVMNTEFEFLIDPQENLVLEITLMDANYMDELTGATFTVSSMKVGEKREY 120
QY 121 PRIFNVQVTEVLEMSLEVCSCPDRLRFSMALCQEKFRQORKEHRESKAKLLGPNNSG 180
Db 121 PRIFNVQVTEVLEMSLEVCSCPDRLRFSMALCQEKFRQORKEHRESKAKLLGPNNSG 180
QY 181 LHSARDVPVALLSGSGGFRAMVGFSGVAKALYESGILDCATYVAGLSSTWMTSLYSH 240
Db 181 LHSARDVPVALLSGSGGFRAMVGFSGVAKALYESGILDCATYVAGLSSTWMTSLYSH 240
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Db 241 PPRPEKGPPEINDELMKNVSHNPLLLTPQKRYVESLMKKSSGQPYTFDIFGMLIG 300
QY 301 ETLIHRMNTTSLSKKNTAQCPLFTCLHVKPDVSELPMADVVESSPEIGAKKG 360
Db 301 ETLIHRMNTTSLSKKNTAQCPLFTCLHVKPDVSELPMADVVESSPEIGAKKG 360
QY 361 TEMAPDLFGSKFFMGTVVAKYEENPLHFLMGVGSASFILFNVLGSGSGSGSTMEBE 420
Db 361 TEMAPDLFGSKFFMGTVVAKYEENPLHFLMGVGSASFILFNVLGSGSGSGSTMEBE 420
QY 421 LENITTKHIVSDSDSDSDSHBPKGTENEDAGSDYOSDNQSWIHRMIALVSDALFN 480
Db 421 LENITTKHIVSDSDSDSDSHBPKGTENEDAGSDYOSDNQSWIHRMIALVSDALFN 480
QY 481 TREGRAGKHNMFLGNTLNTSYPLSPLSDPATQDSFDDDELAAVADPDEFERIYELDV 540
Db 481 TREGRAGKHNMFLGNTLNTSYPLSPLSDPATQDSFDDDELAAVADPDEFERIYELDV 540
QY 541 KSKKIHVDSGLTFNLPYLILRPGQVDLLISFDSARPSSSPPEKELLAEKAKKN 600
Db 541 KSKKIHVDSGLTFNLPYLILRPGQVDLLISFDSARPSSSPPEKELLAEKAKKN 600
QY 601 KLPFRIDYVDRGLACQYFKPKNPMEKDCPTIHFVLANINFRKYKAPGVRETE 660
Db 601 KLPFRIDYVDRGLACQYFKPKNPMEKDCPTIHFVLANINFRKYKAPGVRETE 660
QY 661 EEKEIADFIDDPESPFTFNFQYQNAFKRLHDMHFNLTINIDVIEKAMVESTERYR 720
Db 661 EEKEIADFIDDPESPFTFNFQYQNAFKRLHDMHFNLTINIDVIEKAMVESTERYR 720
QY 721 QNPSRCSVLSNVEARFENKEFLSKPKA 749
Db 721 QNPSRCSVLSNVEARFENKEFLSKPKA 749

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RESULT 2
US-08-827-208-3
Sequence 3, Application US/08827208
Patent No. 6025178
GENERAL INFORMATION:

APPLICANT: Chlou, Xue-Chiou C.
APPLICANT: Kramer, Ruth M.
APPLICANT: Pickard, Richard T.
APPLICANT: Sharp, John D.
APPLICANT: Sciflier, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,208
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/014,608
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-3861
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-827-208-3

Query Match
Best Local Similarity 24.8%; Pred. No. 8,1e-58;
Matches 208; Conservative 152; Mismatches 268; Indels 210; Gaps 26;

18.4%; Score 724; DB 3; Length 913;

21 TVVILRATKVTGAFQMDLTPDPYVELEISTPDSRRKTRHFNNDINVMNTEFEFLID 80
Db 145 TVVILRATKVTGAFQMDLTPDPYVELEISTPDSRRKTRHFNNDINVMNTEFEFLID 80
QY 81 PNOENVLEITLMDANYM-DELTGATFTVSSMKKE-----KKEYPFE----- 122
Db 202 ROLKNVMEIKVDDQDLVGTDDPVLVFLDAGTLRAGEFRRESFSLSPGEGRLVEVFRLO 261
QY 123 -----IFNOV-----TEMYL----- 132
Db 262 SLADNGEMLYSNGVLVARELSCLHVQLEFTGPKSSEHRYOLVVGSGCPQASVGTGT 321
QY 133 -----EMLSEVSCPD----- 143
Db 322 FRHCPACWEOELSTRLODAPPEOLKAPLSALPQGVRLVPTSOEPLMVELKREAGL 381
QY 144 -----LRFSMALCDOEKTEFQORKEHRESKAKLLGPNNSGGLSARDVPVALLSGSGGE 199
Db 382 RELAVRGLGFGPAEBOAFILSRKQVVAALROAL--OLDGLQDEDELPVAVIATGGGI 438
QY 200 RAMVGFSGVAKALYESGILDCATYVAGLSGSTMWSTLYSHDPFPEK--GPEEINEELM 256
Db 439 RAMTSLYGQLAGLKEGLDGVSYITGASGSTMALANLYEDEMSQKDLGPTTEL--LK 495
QY 257 KVVSHNPLLLTPQKRYVESLMKKSSGQPYTFDIFGMLIGETLLHNRKNT--TLSL 315
Db 496 TQVTKKKGVLVAPSOLORYROLASRARLGPSCPTNIMA--LINALLHDEPHDKLSDQ 554
QY 316 KEKVNTAQCPLFLFNCILNKH--PDVSELMADVVESSPEIGAKGTFFMAPDLFGSKFFM 374
Db 555 KEKVNTAQCPLFLFNCILNKH--PDVSELMADVVESSPEIGAKGTFFMAPDLFGSKFFM 374
QY 555 KEKVNTAQCPLFLFNCILNKH--PDVSELMADVVESSPEIGAKGTFFMAPDLFGSKFFM 374
Db 555 KEKVNTAQCPLFLFNCILNKH--PDVSELMADVVESSPEIGAKGTFFMAPDLFGSKFFM 374
QY 375 GTVAVKYEENPLHFLMGVGSASFILFNVLGSGSGSGSTMEBE-----ENITTKH 428
Db 615 GTVAVKYEENPLHFLMGVGSASFILFNVLGSGSGSGSTMEBE-----ENITTKH 428
QY 429 IVSNDSDSD-----ESHEPKGTENEDAGSDYOSDNQSWIHRMIALVSDALFNTEBG 484
Db 659 VANOANLDEQVPLIKIEBPSTAGRIA--EFTFD-----LLTWRP 697
QY 485 RAGKVNHPMLGNTLNTSYPLSPLSDPATQDSFDDDELAAVADPDEFERIYELDVKSK 544
Db 698 IAOATHNPLRGLHFKDYFOHP--HFTWKAATLTDGL-----LPSPSPH 742

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COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,809
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/827,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-498-809-3

```

```

Query Match      18.4% Score 724; DB 4; Length 913;
Best Local Similarity 24.8%; Pred. No. 8,1e-58;
Matches 208; Conservative 152; Mismatches 268; Indels 210; Gaps 26;

QY 21 YVVLATVTVTGAFGMDLTPDPYVELFISTTPDSRRKTRHFNNDINPYWNETFEIIL 80
DB 145 YVVLATVTVTGAFGMDLTPDPYVELFISTTPDSRRKTRHFNNDINPYWNETFEIIL 80
QY 81 PNOENVLETIMDANYVM-DELTGATFTVSSMKVE-----KKEVVF-----122
DB 202 ROLKNVMEIKVEQDLVTDVDPVLYLFDAGTLRAGEFRRESLSLSPGEGRLVEFRILQ 261
QY 123 -----IFNOV-----TEWVL-----132
DB 262 SLADRGEMLVNGLVARELSCLHVLQLEETGDKSSEHRYQLVVPSCGEPQASVGTGT 321
QY 133 -----EMSLVCSGCPD-----143
DB 322 FRHCPACWGEELISRLQDAPEBQKAPLSALPSCGVNRLVFTPSQEPILMVELKKEAGL 381
QY 144 -----LAFSALCDQETFRQQRKEHRESMKKILGPKNSEGLHSADVAVYVALGSGGPF 199
DB 382 RELAVLGGFPCAEEQAFISRRQVVAALROAL--OLDGDLQDEDEIPVVAIMATGGGI 438
QY 200 RAWVGSFVWKALYEGSGLIDCATYVAGLSGTFWYNSTLYSHDPPEK---GPEINEELM 256
DB 439 RAMTSIXGQLAGLKEGLDLCVSYITGASGSTYALANLIEDPEMSOKDLAQPTEL---LK 495
QY 257 KVNSHNPLLLLPQKYRVYESLWKKKSSGQPYTFDIFGMLIGETLLINRMT--TLSSL 315
DB 496 TQVTKNKLGLVAPSQLQRYROELARARLGYPCFTNMA--LINEALLHDEPHDLISQ 554
QY 316 KEKVNTAOCPLPLFTCLAHK--PDVSELMAADVVEESPTEIGMAKYTFMAPDLFGSKFTN 374
DB 555 REALSHGQNPPLPYCALNKGOSLITTFEFGWCEFPSPYEVGPKYGAFTPSELFGSEFFM 614
QY 375 GTVVVKYEENPLHFLMGVGAFAFSLFNRLVVGSGSOSRGSFTPEEL-----ENTTKH 428
DB 615 GQLMKRLPESRICEFEGIMSLYA-----ANLDLSLYWASEPQCFWDM 658

```

```

QY 429 IVSNDSDSD-----ESHEPKGTENEDAGSDYQSDNQASWIRHIMALVSDALNTFRGC 484
DB 659 VNRQANLDRKEQVPLKIEEPSTAGRIA--EFFTD-----LLTWP 697
QY 485 RAGKYNEMLGANTSTYLSPLSPDFATODSFDDELDAVADPDEFERIEPLDYKSK 544
DB 698 LQATHNPLRGHFKHNDYQHP--HFSTWKATLLDGL-----PNO-----LTPSEPH 742
QY 545 IHVVDGLTFNLPYPLILRQGVDPDIISFDSARPSSDSSPPFKELLAEKAKNNKLPE 604
DB 743 LCLLDVGYLINTSCPLQPTRDVLDLISLDYNLGA-----FOQLQIGRCQEGITF 797
QY 605 PRIDPYFDPREGKCEYVK--KPNPDMKDCPTIHFVLANINFRKXKAPVPRETEEK 663
DB 798 PPIPSPEEQDLPRECHTFSPTCP---GAPAVLHFLPVSDFREYSAPGV--RRTPEEA 852
QY 664 ELADPFIIDPSPSEFTFQYPNQAFKRLHLMFNNTLNDIVYKEAMVESIEFRQ 721
DB 853 AAGEVNL-SSSDSPYHYTKVTSQEDVDKLLHLTHYCNNOBOLLEALROAVQRRQ 909

```

RESULT 5

```

US-08-890-615-2
Sequence 2, Application US/08890615
Patent No. 6121031
GENERAL INFORMATION:
APPLICANT: Song, Chuanzheng
APPLICANT: Kriz, Ron
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-GAMMA ENZYMES
TITLE OF INVENTION: AND POLYNUCLEOTIDES ENCODING SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,615
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8224
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Active-site
LOCATION: 6..242
FEATURE:
NAME/KEY: Active-site
LOCATION: 366..535
US-08-890-615-2

```

```

Query Match      12.7% Score 499.5; DB 3; Length 541;
Best Local Similarity 27.0%; Pred. No. 1.7e-37;

```



```

; PRIOR APPLICATION NUMBER: 1215/96
; PRIOR FILING DATE: 1996-10-31
; PRIOR APPLICATION NUMBER: PCT/DK97/00490
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 649
; TYPE: PR1
; ORGANISM: Torulaspora delbrueckii
US-09-295-186-18

```

```

Query Match          5.9%; Score 232.5; DB 3; Length 649;
Best Local Similarity 23.0%; Pred. No. 1e-12;
Matches 113; Conservative 76; Mismatches 156; Indels 147; Gaps 20;

```

```

QY 140 SCDP-----LRFSAALCDQDETFRQORKEHRESMKLLGPKN-----SEGLHSARD 186
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 34 SCDEEDINLRQASGSPSDNETEMLKRDVYTRERALSFLDATSNEFSDSLVSOLFASAD 93
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 187 VPVVALIGSGGFRANVGSVWKALY-----SGILDCATYYAGLSGSTMWMT 236
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 94 IPRIAVACSGGGIRAMLSGAGMLAAMDNRDTGANERHGLGLOSTYTLAGLSGNNLVGT 153
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 237 L-----YSHDPPEKGPPEEINEELMKVSHNP---LTLTPQVKRYVESLAKKSSGQP 288
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 154 LANNMNTSVODIVNNMTEDDSIMDISNIINPGCFMIVTTIKRMDHSDAVEGKODAGFN 213
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 289 VRTEDIFGMLIG---ETLIHNMNTTLLSLK---EKVNTAQCPLPLETCLHVRP-----D 337
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 214 VSLTDJRWGRALSTYFPPSLYRGVAVTWSLTRDVEVFQNEFPEPISVADGRPTQIID 273
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 VSELMPADWEPSPYRIGMAKYGTFMAPDL--FGSKFENGTVVKKXENPLHLMGVWS 395
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 274 LKNTVF---EFPFEEFGS-----MDPTLNATTVKYLSTKVSNGEP----- 311
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 396 AFSILENRVLGVSGSRGSTMEELENTTKHIVSNDSSDSDSHPEKGTENEDAGSD 455
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 312 ---VNKGQCVAGYDNTGFM-----GT----- 330
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 456 YOSDNQASWIRHIMALVSDSALFNTREGRAGVHNPMGLNNTSYPLSPDEAT--Q 513
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 331 -----SSSLFN-----QFLQIN-STSLP--SFINKLVYGF 359
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 514 DSFDDELDAVAADPDEFERIEPLDVKSKKI-----HYVDSGL--TENPYLLILRPOR 566
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 360 DDLSEDEDLAIAPNPFKDTSTYQDNFYSKISSESDLYLVDGEGDNQNPVLPVQDER 419
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 567 GVDLIISPFESA 578
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 420 NVDVIFALDNESA 431
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 8
US-09-295-186-16
; Sequence 16, Application US/09295186B
; Patent No. 6127137

```

```

; GENERAL INFORMATION:
; APPLICANT: Hasida, Miyoko
; APPLICANT: Tsutsuml, No. 6127137iko
; APPLICANT: Halkier, Torben
; APPLICANT: Stlinger, Mary Ann
; TITLE OF INVENTION: An Acidic Phospholipase, Production, and
; TITLE OF INVENTION: Methods of Using Thereof (As Amended)
; FILE REFERENCE: 4953.204-US
; CURRENT APPLICATION NUMBER: US/09/295,186B
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: 1215/96
; PRIOR FILING DATE: 1996-10-31
; PRIOR APPLICATION NUMBER: PCT/DK97/00490
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 18

```

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 612
; TYPE: PR1
; ORGANISM: Penicillium notatum
US-09-295-186-16

```

```

Query Match          5.6%; Score 221.5; DB 3; Length 612;
Best Local Similarity 22.6%; Pred. No. 9.6e-12;
Matches 112; Conservative 78; Mismatches 145; Indels 161; Gaps 24;

```

```

QY 140 SCDPLRFSAALCDQDETFRQORKEHRESMKLLG-----PKNSEGLHSARD 186
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 28 SRPTVSAKLTSTNETSWLEVRGRKTLALKDFGHVKKVGDYVGYLKHSS---GNSSS 84
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 187 VPVVALIGSGGFRANVGSVWKAL-----YESGILDCATYYAGLSGSTMWMS 235
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 85 LPNIGIAVSGGWRALMNGAVKAFDSRTDNATATGHLGLOSTYTYISGLSGSMWLG 144
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 TLVSHDPPE-----KGPEEINEELMKVSHNPILLTLTPQVKRY 275
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 145 STIIN--NFTTVDKLQTHRAGSVQFGNSIIEGPDAGCIQLDSAGT-----YKDL 193
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 276 VESLMKRSKSGQPVFTDIFGMLIGETLI---HNRNNTLLSLKE---KVNTAQCPLPLET 330
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 194 ADAVDKRRAGFDTLTDLMGRALSYQMFNASNGLSYTWSSYADPREFQDGGYPMFPVY 253
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 331 CLHVRPDVSELMF---ADWERSPEYIGMAKYGTFMAPDLFGSKFPMGVVKKYEENPLH 387
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 254 ADGRNP--DELVIGSNSTYVEFNPWE---FGTF--DPTIFG---FV-----PLE 292
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 388 FLKGVGSAFSLIFNVLVGVSGSRGSTMEELENTTKHIVSNDSSDSDSHPEKGT 447
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 293 YL-----GSKFEGSLP-----SNESCIRGDS----- 315
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 448 ENEDAGSDYQSDNQASWIRHIMALVSDSALFNTREGRAGVHNPMGLNNTSYPLSP 507
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 316 ---AG-----FVIGTSSSLFN-----QFLQIN--TSLP--SFI 343
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 508 SDFATQDSFDD--ELDAVADPDEFERIEPLD--VKSKKIHYVDSGLT--FNLPLPLL 562
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 344 KDFENGILFDLKSQNDIASYDPNPFYKYNHSSPYAAOKLLDVYDGGDGNVPLHPLI 403
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 563 RPQGVYDLIISPFESA 578
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 404 QPRHVDVIFAVDSSA 419
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 9
US-09-295-186-17
; Sequence 17, Application US/09295186B
; Patent No. 6127137

```

```

; GENERAL INFORMATION:
; APPLICANT: Hasida, Miyoko
; APPLICANT: Tsutsuml, No. 6127137iko
; APPLICANT: Halkier, Torben
; APPLICANT: Stlinger, Mary Ann
; TITLE OF INVENTION: An Acidic Phospholipase, Production, and
; TITLE OF INVENTION: Methods of Using Thereof (As Amended)
; FILE REFERENCE: 4953.204-US
; CURRENT APPLICATION NUMBER: US/09/295,186B
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: 1215/96
; PRIOR FILING DATE: 1996-10-31
; PRIOR APPLICATION NUMBER: PCT/DK97/00490
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 664
; TYPE: PR1
; ORGANISM: Saccharomyces cerevisiae

```


NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 10
 LENGTH: 552
 TYPE: PRT
 ORGANISM: Hyphozyma sp. CBS 648.91
 US-09-295-186-10

Query Match 5.1%; Score 200.5; DB 3; Length 552;
 Best Local Similarity 21.5%; Pred. No. 6.9e-10;
 Matches 118; Conservative 76; Mismatches 196; Indels 159; Gaps 24;

154 EKTFRQKHEHIESMKLLG-----PKNSEGLHSARD-VPVAILGSGGFRAMV 203
 114 EADYVSRRTNQADAKMKLSDAKLNSLPGASNTSTDRVPRGLFSLSGGLRAML 173
 204 GFGGVKAL-----YESGILDCATYVAGLSGSTMSTLYSHPDPEKGPPEINE 253
 174 VGSGLTLOGFDGRNETANQNGCTGILLQAEYIAGISGSMATASL-----TNNMATQ 226
 254 ELKKNVSHNLLLTLPQ--VKRRYVESLKM---KSSGQVTFETDFGMLIGETLH--- 305
 227 SLADNTIDLESNTLIVPDGKVSFTASTLAAGVGRNNGYQTSLDYFGLSLADKILGSM 286
 306 --NRMTTSLSK--EKVNTAOCPLPLFTCLHVKPDVSELMF---ADWVEFSPEYIGM- 356
 287 YGAKFVSVMGDKVNTSKFTDASMPFIIDNEHP--GELLIRNTIIM-EPNPEYEGSM 343
 357 -AYGTFMADLGSKEFFMGT-----VYKKEENPLHLMGWSABSLRNRYLGV 408
 344 NPVSAEIPLEIGSSLDNCTSVLPDGVCGGYE--TVAWVGTSATLFGSLYLELI--- 398
 409 GSOSRGSTMEELNITTKRIIVSNDSSDDESHPEKGTENEDAGSDYQSDNQASWIRH 468
 399 -STSSNIIYDALKEIA--QAVSNEQND----- 423
 469 IMALVSDSALFNTREGKAGVHNFMLGLNLTSPSLSDFAFDQSFDDDELDAAYADP 528
 424 -VSLVP-----NPFYGVYV-----EGDVQYSD- 444
 529 DEFERITEPDKVSKKHVVDGSL-FTNLFPYLILRPQKQVVDLISDFESARSD--SSP 585
 445 -----LRNTTLVDGGIDNENVPMLPVEPARDLVIALDSSADTMMNPNAS 491
 586 PFKELLAEKWMKMKLPFKI-DPYVDEREGLEKCYVFKPKPMDMKDPTIIEFLIAN 644
 492 ALVQTSIRAGYPTYSOYAFVMPDTNVVNRGLNTRPVF-----YGCNATVYVTNAD 543
 645 INFRKRYKAP 653
 544 TSFNGTKTP 552

RESULT 12
 US-08-609-049A-16
 Sequence 16, Application US/08609049A
 Patent No. 5948664
 GENERAL INFORMATION:
 APPLICANT: Williams, Lewis T.
 APPLICANT: Moitz, Lisa
 APPLICANT: Chen, Yen-Wen
 TITLE OF INVENTION: No. 5948664el PI 3-Kinase Polypeptides
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/609,049A
 FILING DATE: 29-FEB-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Karen B.
 REGISTRATION NUMBER: 29,684
 REFERENCE/DOCKET NUMBER: 2307K-063700US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 140 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-609-049A-16

Query Match 2.8%; Score 112; DB 2; Length 140;
 Best Local Similarity 30.6%; Pred. No. 0.0098;
 Matches 30; Conservative 21; Mismatches 37; Indels 10; Gaps 5;

43 DPVLEFI--STPDSRRKRRHFNNDINPVNTEFF--ILDN-QENVLETIMKAN-Y 96
 47 DPVKKHLPLGASKSMKRLKTLNTRNPIWNETLVHGTDDMKRKTLRISVCEDEXF 106
 97 VMDLETGATFTVSSMKVGEKEVPEIFNQVTEVLEM 134
 107 GHNEFIGETFRSLKLLKPNQRKN----FNICLERVIPM 140

RESULT 13
 US-08-095-737-4
 Sequence 4, Application US/08095737
 Patent No. 5487979
 GENERAL INFORMATION:
 APPLICANT: DiFiore, Pier P
 APPLICANT: Fazio, Francesca
 TITLE OF INVENTION: A Substrate for the Epidermal Growth
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knodde, Martens, Olson & Bear
 STREET: 620 Newport Center Drive, Sixteenth Floor
 CITY: Newport Beach
 STATE: California
 COUNTRY: United States of America
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/095,737
 CLASSIFICATION: 530
 FILING DATE: 19930722
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelson, Ned A.
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: NIH060.001A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 897 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-095-737-4

Query Match 2.7%; Score 108; DB 1; Length 897;
Best local Similarity 20.2%; Pred. No. 0.55;
Matches 100; Conservative 60; Mismatches 203; Indels 132; Gaps 20;

QY 210 KALYESGIL---DCATYVAGLSGSTMWST-----LYSHDPPEKGP----- 248
DB 225 KARYDEIFLTKDMDGYVSGLEVRETFKTLGPSALLAHIMWISLQTKGCKLSKQFAL 284
QY 249 --EINEELMKVNSHNPILLTPQVKRYVESLMKKSSG-QPVTFTDIFGMLIGETL-- 303
DB 285 AFHLINOKLIKGI--DPHSLTPTEMIPPSDRSSLQKNITSSPV--ADFAIKELDTLNN 340
QY 304 ---IHNRMTTSLSLKEKVNFAOCPLEFTCLHVKPDVSELM-FADWVEFSPEYIGMAR 358
DB 341 EIVDLOREKNNVBODLKEKEDT-----VKQRTSEVODLQDEVQRESINLOKIQ 388
QY 359 YGTFMAPDLFGSKFEGTVKKYEENPLHFLMGWGSAPSIENRYLGVSQSGRSTME 418
DB 389 AOKQVOELLGEL---DEQKAOLEQLEVRKKCAEAOILISLKAETISQESQISSYE 444
QY 419 -----ELENITTKHIYVNSDSDSDSHPEKGTENEDAGSDYOS----- 458
DB 445 EELKAREELSRLOQETAOLESEVSGKAOLEPLQOHLQSOEISSMORLEMKDLETD 504
QY 459 DNQASWIRHIMALV---SDSALFNTREGRAKVHNFMLGLNLTSTPLSPLS-----D 509
DB 505 NNOSSNMSSPSQVLYNGATYCSLSTSSSETANFNENAEQNNLESPTHOESSVRSPE 564
QY 510 FARQDSFDDDELDAVA-----DPDEFERIEPLDVSKKI--HYVDSGLTFNLPP 559
DB 565 IASDVTDESEAVTVAGNEKVTFRFDDKHSKEEDPNNVSSSLTDVAADTNLDF----- 619
QY 560 LILRPQGVDLITSPDSARPSDPSPEFKELLLAEKAKNNKLPFPKIDPVYVDRGLKE 619
DB 620 -----FQSDPEVGSDFPKD-----DPFGKIDPFQGD----- 645
QY 620 CYVEFKPNPDMKDC 634
DB 646 --PFGKSDP--FASDC 657

RESULT 14
US-08-480-145-4
; Sequence 4, Application US/08480145
; Patent No. 5717067
; GENERAL INFORMATION:
; APPLICANT: DIFiore, Pier P
; APPLICANT: Fazio, Francesca
; TITLE OF INVENTION: A Substrate for the Epidermal Growth
; FACTOR RECEPTOR KINASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: United States of America
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,145
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/095,737
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelson, Ned A
; REGISTRATION NUMBER: 29,655
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ. ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 897 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-145-4

Query Match 2.7%; Score 108; DB 1; Length 897;
Best local Similarity 20.2%; Pred. No. 0.55;
Matches 100; Conservative 60; Mismatches 203; Indels 132; Gaps 20;

QY 210 KALYESGIL---DCATYVAGLSGSTMWST-----LYSHDPPEKGP----- 248
DB 225 KARYDEIFLTKDMDGYVSGLEVRETFKTLGPSALLAHIMWISLQTKGCKLSKQFAL 284
QY 249 --EINEELMKVNSHNPILLTPQVKRYVESLMKKSSG-QPVTFTDIFGMLIGETL-- 303
DB 285 AFHLINOKLIKGI--DPHSLTPTEMIPPSDRSSLQKNITSSPV--ADFAIKELDTLNN 340
QY 304 ---IHNRMTTSLSLKEKVNFAOCPLEFTCLHVKPDVSELM-FADWVEFSPEYIGMAR 358
DB 341 EIVDLOREKNNVBODLKEKEDT-----VKQRTSEVODLQDEVQRESINLOKIQ 388
QY 359 YGTFMAPDLFGSKFEGTVKKYEENPLHFLMGWGSAPSIENRYLGVSQSGRSTME 418
DB 389 AOKQVOELLGEL---DEQKAOLEQLEVRKKCAEAOILISLKAETISQESQISSYE 444
QY 419 -----ELENITTKHIYVNSDSDSDSHPEKGTENEDAGSDYOS----- 458
DB 445 EELKAREELSRLOQETAOLESEVSGKAOLEPLQOHLQSOEISSMORLEMKDLETD 504
QY 459 DNQASWIRHIMALV---SDSALFNTREGRAKVHNFMLGLNLTSTPLSPLS-----D 509
DB 505 NNOSSNMSSPSQVLYNGATYCSLSTSSSETANFNENAEQNNLESPTHOESSVRSPE 564
QY 510 FARQDSFDDDELDAVA-----DPDEFERIEPLDVSKKI--HYVDSGLTFNLPP 559
DB 565 IASDVTDESEAVTVAGNEKVTFRFDDKHSKEEDPNNVSSSLTDVAADTNLDF----- 619
QY 560 LILRPQGVDLITSPDSARPSDPSPEFKELLLAEKAKNNKLPFPKIDPVYVDRGLKE 619
DB 620 -----FQSDPEVGSDFPKD-----DPFGKIDPFQGD----- 645
QY 620 CYVEFKPNPDMKDC 634
DB 646 --PFGKSDP--FASDC 657

RESULT 15
US-08-477-389-4
; Sequence 4, Application US/08477389
; Patent No. 5872219
; GENERAL INFORMATION:
; APPLICANT: DIFiore, Pier P
; APPLICANT: Fazio, Francesca
; TITLE OF INVENTION: A Substrate for the Epidermal Growth
; FACTOR RECEPTOR KINASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth floor

Search completed: July 31, 2001, 16:30:09
Job time: 56 sec

CITY: Newport Beach
STATE: California
COUNTRY: United States of America
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,389
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/095,737
FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelson, Ned A
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH060,001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 897 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-389-4

Query Match 2.7%; Score 108; DB 2; Length 897;
Best Local Similarity 20.2%; Pred. No. 0.55;
Matches 100; Conservative 60; Mismatches 203; Indels 132; Gaps 20;

OY 210 KALYESGIL---DCATYVAGLSGSTMWST-----LYSHDPPEKGP----- 248
DB 225 KAKYDEIFLTKDKMDGVSGLEVRETFILKGLPSALAHIMSLDTCGCKLSKDOQFAL 284
OY 249 --EINEELMKVSNPLLLLPQAKRYVESLMKKSSG-QPYFTDIFGMLIGETL-- 303
DB 285 APHLINOKLIKGI--DPRHSLTPEMIPPSDRSSLQKNITGSSPV--ADPSAIKELDTLNN 340
OY 304 ---IHNRMNTLSSLIKEVNTACPLPLFTCLHYKPDVSELM--FADWVEFSPYEIGMAK 358
DB 341 EIVDLQREKNNEQDLKEDEI-----VKQRTSEVODLQDEVQRESINLQKLQ 388
OY 359 YGTFMAPDLFGSKFPMGVVKKRYEENPLHFLMGVGSASFILFNRYLGVSGSOSRGSTME 418
DB 389 AOKQOVQELLGEL---DEQKAQLEBQLEVRKKCAEEAQLISLKAETISQESQISSYE 444
OY 419 -----ELENITTKHIYNSDSSDDESHPEKGTENDAGSDYOS----- 458
DB 445 EELLAREELSLRLOQETAGLESVESGKAQLEPLQOHLQESQOELISSMOMRLMKDLETD 504
OY 459 DNQASMIHRIMIALY---SDSALFMTREGRAGKVHNFMLGLNLTSYPLSPUS-----D 509
DB 505 NNQSNMSSSPQSVLVNGATDYCSLSTSSSETANFNEHAGQNNLSEPTHQESSVRSRSP 564
OY 510 FATQDSFDDELDAVA-----DPDEFRIYPLDYKSKRI--HVVDSGLTFNLPYP 559
DB 565 IAPSDVTDESEAVYAAGNEKVTPRFDDDKHSKEEDPFNVNESSLTDVAADTNLDF----- 619
OY 560 LILRQRGVDLIIISFDSARPSDSSPPREKELLAEKMAKMKLPPPKIDPYVFDREGLKE 619
DB 620 -----FQSDPFVGSDDPFKD-----DPFGKIDPFEGD----- 645
OY 620 CYVEKPKNDPMKDC 634
DB 646 --PFKGSDF--FASDC 657

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 31, 2001, 16:29:13 ; Search time 22.62 Seconds
(without alignments)
2007.399 Million cell updates/second

Title: US-09-250-083A-2

Sequence: 1 MSFIDPYQHIVEHQYSHKF.....LSNVEARRFFNKEFLSKPKA 749

Scoring table:

	BLOSUM62	
Canoe 10 0		Canoe 0 0

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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2	/SIDS8/gcgdata/genseq/genseq/AAL1982.DAT *
3	/SIDS8/gcgdata/genseq/genseq/AAL1983.DAT *
4	/SIDS8/gcgdata/genseq/genseq/AAL1984.DAT *
5	/SIDS8/gcgdata/genseq/genseq/AAL1985.DAT *
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22	/SIDS8/gcgdata/genseq/genseq/AAL2002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3942	100.0	749	13	AA826501	Cytosolic phosphol
2	3942	100.0	749	15	AA863757	Human phospholipas
3	3942	100.0	749	17	AA897751	Human phospholipas
4	3942	100.0	749	18	AAW11607	Human phospholipas
5	3942	100.0	749	18	AAW11650	Human phospholipas
6	3942	100.0	749	21	AAV58631	Human phospholipas
7	3935	99.8	749	15	AA854090	Human phospholipase
8	3224	81.8	611	21	AA821142	Human cytosolic ph
9	724	18.4	913	21	AAV51557	Human PL2A protein
10	724	18.4	913	22	AA874635	Phospholipase A2 (
11	663	16.8	533	21	AA821140	Human cytosolic ph

12	619	15	7	605	21	AAH03628
13	608	15	4	483	19	AAH75132
14	608	15	4	483	19	AAH75067
15	499	12	7	541	21	AAH82897
16	494	12	5	541	21	AAH79388
17	482	12	2	551	21	AAH31141
18	441	11	2	135	15	AAH63758
19	436	11	1	135	17	AAH97752
20	433	11	0	135	18	AAH11651
21	431	10	9	135	18	AAH44651
22	428	10	9	135	15	AAH76660
23	289	7	3	654	21	AAH71236
24	272	6	9	648	21	AAH71237
25	201	5	1	573	19	AAH48874
26	200	5	1	573	19	AAH48873
27	172	5	4	285	21	AAH51976
28	172	5	4	287	21	AAH51975
29	172	5	4	337	21	AAH51974
30	138	3	5	773	21	AAH35474
31	136	3	5	776	21	AAH43548
32	129	3	5	718	21	AAH43549
33	125	3	2	1096	17	AAH01556
34	125	3	2	794	15	AAH74421
35	121	3	1	999	21	AAH33685
36	121	3	1	1008	21	AAH33684
37	111	3	1	1065	21	AAH33683
38	112	2	8	26	13	AAH22090
39	111	2	8	1186	16	AAH50645
40	110	2	8	400	17	AAH01114
41	110	2	8	503	20	AAH63432
42	110	2	8	503	16	AAH72365
43	110	2	8	503	17	AAH33170
44	110	2	8	503	17	AAH1464
45	110	2	8	503	20	AAH05202

ALIGNMENTS

RESULT 1

ID AAR26501 standard; Protein; 749 AA.

AC AAR26501;

DT 10-MAR-1993 (first entry)

DE Cytosolic phospholipase A2.

KW CPLA2; recombinant; inhibitors; phosphatide 2-acylhydrolase.

OS Homo sapiens

PN EP509719-A.

PD 21-OCT-1992

PF 10-APR-1992; 92EP-0303209

PR 17-APR-1991; 91US-0686558.

PA (ELLIL) LILLY & CO ELLI.

PI Chiou XC, Hoskins JA, Kramer RM, Sharp JD, White DL,

DR WPI; 1992-351356/43.

XX

PT useful in screening of compounds for cPLA2 inhibitors

PS Disclosure; Page 13-15; 27pp; English.

CC Phospholipase A2 (PLA2) is the common name for phosphatide-2-
 CC acylhydrolase which catalyses the hydrolysis of the sn-2 acyl ester
 CC bond of phosphoglycerides. The most abundant form of PLA2 is the
 CC secreted form. Cytosolic PLA2 is extremely rare so an expression
 CC system was developed to yield larger amts. of the enzyme, which is
 CC thought to be involved in asthma, ischemia, arthritis, septic shock
 CC and inflammatory diseases of the skin. The cDNA sequence of cPLA2
 CC was enzymatically copied from the mRNA found in nature (see
 CC US92301620.8 for details). The cDNA may be inserted into an
 CC expression vector, pref. contg. a promoter, a selectable marker,
 CC a temp. sensitive repressor and other regulatory elements necessary
 CC for transcription and translation in E. coli. The vector may be
 CC used to transform E. coli, which may be cultured to obtain large amts.
 CC of cPLA2. The gene, and the enzyme it encodes may be used to
 CC screen cpds. to identify inhibitors of cPLA2.

XX Sequence 749 AA:

Query Match 100.0%; Score 3942; DB 13; Length 749;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFTDPYQHIIYEHQYSHKFTYVVLRAVTYKAGFDMLEDPDYVELFISTTPDSRKRT 60
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 QY RHNNNDINVMNTEFEELIDPNQENLETTIMDANYMETLGTAFYTSMKVGEKKEY 120
 DB 61 rhnnndinvmntefelidpnqenvleltlmdanymetlgtafytsmkvgekkey 120
 QY 121 PFIENOVTEVLEMSLEVCSPDLRFSMALCDQEKTFROORKEIHESMKKLGPKNSE 180
 DB 121 pfienovtevmlemslevcspdlrfsmalcdqektfroorkeihesmkklgpnkse 180
 QY 122 pffingvtemvlemalesvcspdlrfsmalcdqektfgrkhesmkklgpnkse 180
 DB 122 pffingvtemvlemalesvcspdlrfsmalcdqektfgrkhesmkklgpnkse 180
 QY 181 LHSARVPYVAILGSGGFRAYGSGVMKALYESGILDCAITYAGLSGTYWSTLYSH 240
 DB 181 lhsarvpvvaillgsggfraygsgvmkalysesgildcaityaglsgstywstlysh 240
 QY 181 lhsarvpvvaillgsggfraygsgvmkalysesgildcaityaglsgstywstlysh 240
 DB 181 lhsarvpvvaillgsggfraygsgvmkalysesgildcaityaglsgstywstlysh 240
 QY 241 PDPEPEKPEINEELMKNSHNPILLTLTPQKRYVESLWKKSSQPVLCFIDFIMLI 300
 DB 241 pdpepekpeineelmknsnhnpilltltpqkryveslwkssqpvvlcfdifmli 300
 QY 241 pdpepekpeineelmknsnhnpilltltpqkryveslwkssqpvvlcfdifmli 300
 DB 241 pdpepekpeineelmknsnhnpilltltpqkryveslwkssqpvvlcfdifmli 300
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 QY 301 etlihnrmntlslekynvtaqcplpftclhvkpdsvelmfadwvetspyeigmaky 360
 DB 301 etlihnrmntlslekynvtaqcplpftclhvkpdsvelmfadwvetspyeigmaky 360
 QY 361 TFMAPDLFGSKFTFMGTIVKKEBNPLHFLMGWGSAPSLFNRYLGVSGSOSRGSTME 420
 DB 361 tfmapdlfgskftfmgtivkkyeepnlhflmgwgsasfslfnrylgvsgsrgstme 420
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 DB 361 tfmapdlfgskftfmgtivkkyeepnlhflmgwgsasfslfnrylgvsgsrgstme 420
 QY 421 LENITTKHIVNSDSDSDSHPEKGTENDAGSDYQSDNOASWIRHMLMALVSDSALFN 480
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 QY 421 lenittkhivnsdssdshpekgtendagsdyqsdnoaswirhmlmalvdsalfn 480
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 DB 481 tregragkvhnmflgintsyplspdsdfatqdsfdddeldaavadpdeferyel 540
 QY 481 tregragkvhnmflgintsyplspdsdfatqdsfdddeldaavadpdeferyel 540
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 QY 541 KSKKIVVNSGLTFNLPLYILARPGVDLIISFDSAPSDSPFFKELLAEKAKANN 600
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 DB 541 kskkivvnsgltfnlplyilarpogvdliisfdsapssdpffkellaeakann 600
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 QY 661 EKEKELADFIDDPESPSTFSTFNQYNOAFKRLHDLMHENTLNINIDIVIEAMVESTI 720
 DB 661 eekeladfidddpespfstfnqynoafkrlhldlmhntlnnidivieamvesti 720
 QY 661 eekeladfidddpespfstfnqynoafkrlhldlmhntlnnidivieamvesti 720
 DB 661 eekeladfidddpespfstfnqynoafkrlhldlmhntlnnidivieamvesti 720
 QY 721 QNPSRCVSLSNVEARRFENKEFLSKPKA 749
 DB 721 qnpsrcvslsnvearrfenkeflskpka 749

DB 721 qnpsrcvslsnvearrfenkeflskpka 749

RESULT 2

ID AAR63757 standard; Protein; 749 AA.

AC AAR63757;

DT 09-JUN-1995 (first entry)

XX Human phospholipase A2 (PLA2).

XX Intracellular phospholipase A2; PLA2; anti-inflammatory chemicals;

XX prostaglandin leukotriene regulation; platelet activating factor.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 414..427
 /note="tryptic fragment used to design the oligonucleotides"

FT Peptide 534..0
 /note="tryptic fragment"

FT Peptide 599..601
 /note="tryptic fragment"

FT Peptide 607..613
 /note="tryptic fragment"

FT Peptide 649..656
 /note="tryptic fragment used to design the oligonucleotides"

FT Peptide 710..718
 /note="tryptic fragment"

PN US5354677-A.

XX 11-OCT-1994.

XX 28-FEB-1990; 90US-0486628.

XX 28-FEB-1990; 90US-0486628.

XX 13-JAN-1993; 93US-0002447.

XX (GENY) GENETICS INST INC.

XX Clark J, Knopf JL;

XX WPI: 1994-324553/40.

XX N-PSDB: AA074416.

XX Intracellular phospholipase A2 - used in methods for detecting

XX the anti-inflammatory potential of various chemical agents

XX Claim 1; Columns 5-10; 13pp; English.

XX The cDNA sequence AA074416 encodes AAR63757, biologically active

XX human phospholipase A2 (PLA2). This enzyme can be used to

XX determine the anti-inflammatory potential of various chemical

XX agents. PLA2 also displays enzymatic activity in a mixed micelle

XX assay, this activity indicates PLA2's involvement in the regulation

XX of the prostaglandin and leukotriene pathways, and the biosynthesis

XX of platelet activating factor.

SO Sequence 749 AA:

Query Match 100.0%; Score 3942; DB 15; Length 749;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFTDPYQHIIYEHQYSHKFTYVVLRAVTYKAGFDMLEDPDYVELFISTTPDSRKRT 60
 DB 1 msftldpyghilvehgshkftvvlratkvkgaifgdmldpdpvvelfsttpdsrkr 60

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Db 61 rhfnndinpwntefeiildpnoenvleitmdaymdeitlgatftvssmkvgekev 120
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XX 121 pftfnqvtewvlekslvgvscpdrlrfsmalcdqkftfrqqrkehiresmkllgpknsseg 180
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Db 181 lhsardvpvvaaiigsggffamvfgsgvmkalysesgildcatyvagisgstwmwstlysh 240
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XX 241 pdpekgpbeinebelmkvsnhnpilltpokvrkyveslkkkssgqpvftdifgmlig 300
Db 241 pdpekgpbeinebelmkvsnhnpilltpokvrkyveslkkkssgqpvftdifgmlig 300
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Db 301 etlihnrmnttslkrvntaqcplplftclhvkrpvselmfadwvespyeigmakyg 360
QY 361 TFMAPDLFGSKFPMGTAVKKYEENPLHFLMGVMSAFSILFNRYLGVSQSRSSTMEEE 420
XX 361 tfmapdlfgskfpmgtavkkyeenplhflmgvmsafsilfnrylgvsqsrsstmeeee 420
Db 361 tfmapdlfgskfpmgtavkkyeenplhflmgvmsafsilfnrylgvsqsrsstmeeee 420
QY 421 LENITTKHIVSNDSDSDSHPEKGTENEDAGSDYOSDNQASWIRHMALVSDSALFN 480
XX 421 lenittkhivsndsdsdshpekgtenedagsdyosdnqaswirhmalvdsalfn 480
Db 421 lenittkhivsndsdsdshpekgtenedagsdyosdnqaswirhmalvdsalfn 480
QY 481 TRGRACKVHNFMGLNLTSTPLSDPATQDSFDDDELDAVADPDERIYERLDV 540
XX 481 trgrackvhnfmglntstplsdpatqdsfdddelдаваддерийерлдь 540
Db 481 trgrackvhnfmglntstplsdpatqdsfdddelдаваддерийерлдь 540
QY 541 KSKKIHVVDGILFENLIPYLILRQRGVDLISDFGARSDDSPPKELLAEKAKMN 600
XX 541 kskkihvvdsgilfenlipylilrqrgvdlisdfgarsddspkellaeakamn 600
Db 541 kskkihvvdsgilfenlipylilrqrgvdlisdfgarsddspkellaeakamn 600
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Db 721 qnpsrcsvslsnyearfefekpelskpk 749

```

RESULT 3

AAR97751
ID AAR97751 standard; Protein: 749 AA.

XX AAR97751;

XX 28-AUG-1996 (first entry)

XX Human phospholipase A2.

XX Phospholipase A2; PLA2; antiinflammatory.

XX Homo sapiens.

XX US5527698-A.

XX 18-JUN-1996.

XX 28-FEB-1990; 90US-0486628.

XX 28-FEB-1990; 90US-0486628.

XX 13-JAN-1993; 93US-0002447.

XX 22-JUN-1994; 94US-00263861.

```

XX (GEM ) GENETICS INST INC.
PA Clark J, Knopf JL;
XX WPI; 1996-299858/30.
DR N-PSDB; AAR29822.
XX
PT Purified mammalian cytosolic phospholipase A2 - useful to identify
XX anti-inflammatory cpds.
PS Claim 1; Column 5/6-9/10; 13pp; English.
XX
CC A cytosolic phospholipase A2 (PLA2) (AAR29822) was identified as
CC the product of a cDNA clone (AAR29822) isolated from a cDNA
CC library derived from human U937 cells. The PLA2 can be
CC expressed in transformed or transfected bacterial, yeast, mammalian
CC or insect host cells. The specific activity of the PLA2 is approx.
CC 20 umol/min.mg in the mixed micelle assay. The enzyme is useful
CC for identifying antiinflammatory cpds. by determining if the cpd.
CC inhibits PLA2 in cleaving a phospholipid to release fatty acids
CC in a mixed micelle assay, a system using natural enzymes or in
CC whole cells overexpressing the enzyme.
XX
SQ Sequence 749 AA:
XX
Query Match 100.0%; Score 3942; DB 17; Length 749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFIDPYOHAIIVEHOYSHKFTVVVLRAATKYTKGAFGMDLTPDPYVELFISTTPDSHKRT 60
XX 1 msfidpyohaiivehoyskhftvvvlraatkytkgafgmdltpdpyselsttpdshkrt 60
Db 1 msfidpyohaiivehoyskhftvvvlraatkytkgafgmdltpdpyselsttpdshkrt 60
QY 61 RHEFNNDINPWNTEFEIILDPNOENVLEITLMDANYMDETLGATPTVSSMKGEKKEV 120
XX 61 rhfnndinpwntefeiildpnoenvleitmdaymdeitlgatftvssmkvgekev 120
Db 61 rhfnndinpwntefeiildpnoenvleitmdaymdeitlgatftvssmkvgekev 120
QY 121 PFTFNQVTEWVLEKSLVGVSCPDRLRFSMALCDQKFTFRQQRKEHIRESMKLLGPKNSEG 180
XX 121 pftfnqvtewvlekslvgvscpdrlrfsmalcdqkftfrqqrkehiresmkllgpknsseg 180
Db 121 pftfnqvtewvlekslvgvscpdrlrfsmalcdqkftfrqqrkehiresmkllgpknsseg 180
QY 181 LHSARDVPVVAIIIGSGGFFAMVGFSGVMKALYESGILDCATYVAGISGSTMWSTLYSH 240
XX 181 lhsardvpvvaaiigsggffamvfgsgvmkalysesgildcatyvagisgstwmwstlysh 240
Db 181 lhsardvpvvaaiigsggffamvfgsgvmkalysesgildcatyvagisgstwmwstlysh 240
QY 241 PDPEKGPBEINBELMKVSNHNPILLTPOKVRKYVESLKKKSSGQPVFTDIFGMLIG 300
XX 241 pdpekgpbeinebelmkvsnhnpilltpokvrkyveslkkkssgqpvftdifgmlig 300
Db 241 pdpekgpbeinebelmkvsnhnpilltpokvrkyveslkkkssgqpvftdifgmlig 300
QY 301 ETLIHNRMNTTSLKRVNTAQCPLPLFTCLHVKRPVSELMFADWVESPYEIGMAKYG 360
XX 301 etlihnrmnttslkrvntaqcplplftclhvkrpvselmfadwvespyeigmakyg 360
Db 301 etlihnrmnttslkrvntaqcplplftclhvkrpvselmfadwvespyeigmakyg 360
QY 361 TFMAPDLFGSKFPMGTAVKKYEENPLHFLMGVMSAFSILFNRYLGVSQSRSSTMEEE 420
XX 361 tfmapdlfgskfpmgtavkkyeenplhflmgvmsafsilfnrylgvsqsrsstmeeee 420
Db 361 tfmapdlfgskfpmgtavkkyeenplhflmgvmsafsilfnrylgvsqsrsstmeeee 420
QY 421 LENITTKHIVSNDSDSDSHPEKGTENEDAGSDYOSDNQASWIRHMALVSDSALFN 480
XX 421 lenittkhivsndsdsdshpekgtenedagsdyosdnqaswirhmalvdsalfn 480
Db 421 lenittkhivsndsdsdshpekgtenedagsdyosdnqaswirhmalvdsalfn 480
QY 481 TRGRACKVHNFMGLNLTSTPLSDPATQDSFDDDELDAVADPDERIYERLDV 540
XX 481 trgrackvhnfmglntstplsdpatqdsfdddelдаваддерийерлдь 540
Db 481 trgrackvhnfmglntstplsdpatqdsfdddelдаваддерийерлдь 540
QY 541 KSKKIHVVDGILFENLIPYLILRQRGVDLISDFGARSDDSPPKELLAEKAKMN 600
XX 541 kskkihvvdsgilfenlipylilrqrgvdlisdfgarsddspkellaeakamn 600
Db 541 kskkihvvdsgilfenlipylilrqrgvdlisdfgarsddspkellaeakamn 600
QY 601 KLPEPKIDPVFDREGLEKCYVEFKPNPDMEKDCPTIIHFVLAININRKYKAPGVPRETE 660
XX 601 klpepkidpvfdreglekyvefkpnpdmekdcpitiihfvlaininrkykagpvprete 660
Db 601 klpepkidpvfdreglekyvefkpnpdmekdcpitiihfvlaininrkykagpvprete 660

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Db 601 klpfkipdyvidreglkecyvfkpnpdmekdcptllhfvlaanlfrkykagpyvprete 660
OY 661 EEKEIADFDIDDPESPSTFNFOYPNQAFKRRLHDLMHENTLNINIDVIKEAWESTIEYR 720
Db 661 eekeiadfdiddpespsftfnfypnqafkrllhdmhntlnnidvikeawestieyrr 720
OY 721 QNPSRCSVSLSNVEARFRFNKEFLSKPKA 749
Db 721 qnprrcsvalsnvearrrfnkelaskpka 749

RESULT 4
AAW11607
ID AAW11607 standard: Protein; 749 AA.
AC AAW11607;
DE 07-OCT-1997 (first entry)
DE Human phospholipase A2 enzyme.
DE Human; PLA2; anti inflammatory; drug development; antibody.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 414..427
FT Region /label= Tryptic_fragment
FT Region 534..540
FT Region /label= Tryptic_fragment
FT Region 599..601
FT Region /label= Tryptic_fragment
FT Region 607..613
FT Region /label= Tryptic_fragment
FT Region 649..656
FT Region /label= Tryptic_fragment
FT Region 710..718
FT Region /label= Tryptic_fragment

US5593878-A.
PN 14-JAN-1997.
PF 28-FEB-1990; 90US-0486628.
PR 28-FEB-1990; 90US-0486628.
PR 13-JAN-1993; 93US-0002447.
PR 22-JUN-1994; 94US-0263590.
PA (GENW ) GENETICS INST INC.
PI Clark J, Knopf JL;
PI MPI: 1997-099471/09.
PI N-PSDB; AAT61187.
PT New murine phospholipase A2 enzymes - useful for developing
PT anti-inflammatory drugs
PS Example 4; Column 5-8; 22pp; English.
XX The present sequence represents human phospholipase A2 enzyme (PLA2).
XX The human sequence shares significant similarity to protein kinase
XX C-gamma, indicating a common function. The function is likely to include
XX the regulation of the enzyme by calcium and the calcium dependent
XX binding to membranes. The tryptic fragments, indicated in the features
XX table, were subjected to automated gas phase microsequencing as part of
XX the protein sequencing analysis of the human PLA2. The PLA2 enzyme is
XX used for detecting the anti-inflammatory potential of various chemical
XX agents, and for developing new drugs. Antibodies to PLA2 may be used
XX diagnostically, in research and for treating inflammatory conditions.
SQ Sequence 749 AA.
```

```
Query Match 100.0%; Score 3942; DB 18; Length 749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSFIDPYQHIIIEHOYSHKFTVVLVLRATKVTGAFGDMLDTPDYPVEFLISTTPDSRKT 60
Db 1 msfidpyqhliivehgyshkftvvlvratkvtkgafgdmldtpdypvellisttpdsrkt 60
OY 61 RHFNNDINFWNETFEFLIDPNOENVLETTMDANYWDETGTATFYSSKAKVEKKEV 120
Db 61 rhfnndinfwnetfeellidpnoenvleltmdanywdetgtatfyssmkvgekkev 120
OY 121 PFENOVTEWVLEMSLEVCSCPDLRFSNALCDEKTEFROCKEHTRESKTKLGFKNSEG 180
Db 121 pfenovtevwlemlslevscpdllrfsmalcdekterfqrkhehresmkkllgfknsseg 180
OY 181 LHSARDVPVVAITLGGSGFRAMVGSVKKALYESGILDCATYVAGLSGTYWNSTLYSH 240
Db 181 lhsardvpvvaillgsggframvgsvkkalysesgildcatyvaglsgstywmsltlysh 240
OY 241 PDPEKGPBEINDELKKNVSHNPDLTLTPQKRYRYVESLMKKSSGQPTFTDIDGMLIG 300
Db 241 pdpekgpbeinelkknvshnpdltltpqkvkryveslmkksqgqptftdldgmlig 300
OY 301 ETLIHRMNTTSLSEKKNYTAQCPLEFTCLHVRPDVSELNFADWVERSPYEIGMAKYG 360
Db 301 etlihrmnttsslsekknvtaqcpleftclhvrpdvselnfnadwverspyeigmakyg 360
OY 361 TFWAPDLFGSKFFPMGTIVVKKYEBNPLHFLMGVGSASFILFNRLVCGVSGOSRGSTMEBE 420
Db 361 tfwapdlfgskffpmgtivvkkkyebnplhflmgvgsasfiflfnrlvlgvsgsrgstmebe 420
OY 421 LKNITTKHIVSDSSDSDESHPEKGTENEDAGSDVQSONQASWIRMTMALVVSALFN 480
Db 421 lknittkhivsdssdsdeshepkgtenedagsdvqsonqaswlrmtmalvvsalfn 480
OY 481 TREGRAGKVNFMGLNLNTSYPLSPDFAVQDSFDDDELAAVADPDEFERIEPLDV 540
Db 481 tregragkvnmfmglnlntsyplspdfavqdsfdddelaaavadpdeferiepldv 540
OY 541 KSKKIHVDSGLTFNIPYLLIRPQGVLLIISFDSNAPSSSPPEKLLLAEKWAKKN 600
Db 541 kskkihvdsgltnipyllirpqgvllisfdsnapspppeklllaekwakkn 600
OY 601 KLPFPKIDPYVDREGIKCYVFKPNPMEKDCPTIIHFVLANINFRKAKAGVPRETE 660
Db 601 klpfpkipdyvidreglkecyvfkpnpmekdcptllhfvlaanlfrkykagpyvprete 660
OY 661 EEKEIADFDIDDPESPSTFNFOYPNQAFKRRLHDLMHENTLNINIDVIKEAWESTIEYR 720
Db 661 eekeiadfdiddpespsftfnfypnqafkrllhdmhntlnnidvikeawestieyrr 720
OY 721 QNPSRCSVSLSNVEARFRFNKEFLSKPKA 749
Db 721 qnprrcsvalsnvearrrfnkelaskpka 749

RESULT 5
AAW14650
ID AAW14650 standard: Protein; 749 AA.
AC AAW14650;
DE 28-JUL-1997 (first entry)
DE Human phospholipase A2 (PLA2).
DE Phospholipase A2; PLA2; inhibitor; inflammation;
DE antiinflammatory.
OS Homo sapiens.
```

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XX Key Location/Qualifiers
FH Peptide 414..427
FT /label- tryptic_peptide-1
FT 534..540
FT Peptide /label- tryptic_peptide-2
FT 599..601
FT Peptide /label- tryptic_peptide-3
FT 607..613
FT Peptide /label- tryptic_peptide-4
FT 649..656
FT Peptide /label- tryptic_peptide-5
FT 710..718
FT Peptide /label- tryptic_peptide-6
XX
XX US562832-A.
XX PD 22-APR-1997.
XX PF 28-FEB-1990; 90US-0486628.
XX PR 28-FEB-1990; 90US-0486628.
XX (GENM ) GENETICS INST INC.
XX PA Clark J, Knopf JL;
XX PI
XX DR MPI: 1997-244389/22.
XX DR N-PSDB; AAT61758.
XX PT Screening assay for phospholipase A2 inhibitors - using
XX PT phospholipase A2 encoded by defined DNA sequence
XX PS
XX PS Claim 1; Columns 5-8; 12pp; English.
XX CC A human phospholipase A2 (PLA2) (AAW14650) has a specific activity
XX CC of 20 umol/min/mg in mixed micelle assay. It can be produced in
XX CC mammalian, insect or bacterial hosts utilizing a cDNA clone
XX CC (AAT61758) obtd. from a human monocyte U937 cDNA library using probes
XX CC based on human PLA2 tryptic peptides (see also AAW14652-56). Human
XX CC and murine PLA2 (see also AAW14651) can be used in screening assays
XX CC for cpds. capable of inhibiting the action of PLA2 in cleaving a
XX CC phospholipid to release fatty acids. Such inhibitory activity is
XX CC indicative of use as an antiinflammatory.
XX CC
XX SO Sequence 749 AA:

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Query Match 100.0%; Score 3942; DB 18; Length 749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MSFTIDYOHITVHOYSKRTVVVLRATKTKGAFGMDLPDYVELFSTPDSKRT 60
DB 1 msftidyghivghyskrtvvlratkvtkgafigmdltpdyvelfstpdsrkt 60
QY 61 RHFNDINPWNTEFFFIIDPNOENVLETIMDANYMDETLGATFTVSMKVGKEKY 120
DB 61 rhfndinpwmetfelfidpngenveltlimdanymetlgtatftvsmvgekev 120
QY 121 PFIPOVTEKMLESLVSCDPLRFSMALCDDEKTFRQGRKHIRESMKLLGPKNSEG 180
DB 121 pfifndynwmetfelfidpngenveltlimdanymetlgtatftvsmvgekev 180
QY 181 LHSARVPVVAITIGSGGFAPAMGFGVGMKALYESGTLDCATVAGISGSSTWSTLYSH 240
DB 181 lhsarvpvvaillgsggfapamgfgsvymkalyesgilldcavaglsgstwstlysh 240
QY 241 PDPEKGPPEINELMKKNVSHNPLLLTPQKRVYESLKKKKSGQPVFTTIFGMLIG 300
DB 241 pdpekgppeeinelmkknvshnp111tpqkvrryeslkkkssgspvfttdlfgmlig 300
QY 301 ETLIHNRNMTTSSLSKEKVTACPLPLFTCLHVKRPDVSELMFADWVEFSPEYELGMAYG 360

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DB 301 etlihnrmntlsslskekvtacp1plftclhvkpdselmadvetspeylgmakyg 360
QY 361 TFWAPDLFGSKTFPMGTIVYKKYEENPLHFLMGVWGSFSLFNFNLGVSGSQSGSTMEEE 420
DB 361 tfwapdlfgsktfpmgtivvykkyeenplhflmgvwsfslfnnfvlvsgsgstgsmee 420
QY 421 LENITTKHIVNDSDDSHHEPKGTENEDAGSDYQSDNQASWIRMTALVSDSALFN 480
DB 421 lenitckhivndssddshhepkgtenedagsdyqsdnqaswlhrrmtalvdsalfn 480
QY 481 TREGKAGKYNHFMGLNLTSTYPLSDFAVDSTDDDELDAVAADPPEFEKITYEPLV 540
DB 481 tregragkynhfmglntstyp1sdlstardtsiddeldaaavdpdeferyepllv 540
QY 541 KSKKHVVDGSLFENLPYPLILRPGVDYLIISFDSARPSSDPPEKELLAEKAKANN 600
DB 541 kskkhvvdsglfnlpypl1lpgvdl1isfd1sarpsdsppekellaeakann 600
QY 601 KLPFKIDPYVEDREGIJEKCYEYKPKRNPMKDCPTIIHFLVAINFRKRYKAPGPRETE 660
DB 601 klpfkidyvfdreglkecyekpknpmekdcptliihflvanlfrkykapyrete 660
QY 661 EEKEIADFDIDPESPESTFNFQYPRQAFLHJLHMTLNNIDVYKAWESTIEYR 720
DB 661 eekeiadfdiddpespfstfnfypnqafkrlhdmhmtlnnidv1kewesleyr 720
QY 721 QNPSCSVLSNVEARFPFKELSKPKA 749
DB 721 qnpscsvlsnvearffnkelskpk 749

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RESULT 6

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ID AAY59631 standard; Protein; 749 AA.
XX AAY59631;
AC AAY59631;
XX
XX 23-MAR-2000 (first entry)
DB
XX Human phospholipase A2 group IV protein sequence.
XX
XX Phospholipase A2 group IV; PLA2; antisense compound; inhibit; tumour;
XX infection; inflammation.
XX
XX Homo sapiens.
XX
XX US6008344-A.
XX
XX 28-DEC-1999.
XX
XX 23-FEB-1999; 99US-0255893.
XX
XX 23-FEB-1999; 99US-0255893.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowser LM;
XX
XX MPI: 2000-086226/07.
XX N-PSDB; AAZ56051.
XX
XX Antisense oligonucleotides inhibit expression of human phospholipase A2
XX group IV, useful for diagnosis, treatment and prevention of tumours,
XX infection and inflammation -
XX
XX Disclosure: Column 41-46; 32pp; English.
XX
XX This is the human phospholipase A2 (PLA2) group IV protein sequence.
XX Phospholipase A2 group IV is activated in response to extracellular
XX stimuli, including growth factors, cytokines, and interferons. The
XX invention relates to an antisense compound which is targeted to the
XX coding region or 5' or 3' untranslated region of PLA2 group IV nucleotide

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CC sequence. The antisense compound inhibits the expression of PLA2 group
CC IV. The PLA2 group IV antisense compounds are used to inhibit the
CC expression of cytosolic PLA2 in cells and tissues in vitro. The antisense
CC molecules can also be used to treat or prevent PLA2-associated diseases,
CC particularly infection, inflammation and tumours. The antisense compound
CC can also be used for research or diagnosis, e.g. to study gene function
CC or in hybridization assays.

SQ Sequence 749 AA:

Query Match 100.0%; Score 3942; DB 21; Length 749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MSFIDPYOHIIYEHQSHKFTYVVLARATVTKGAFGMDLPDPYVELFISTPDSSRKT 60
   |||
Db 1 msfidpyghllvehyshkftvvlratkvkgaigdmldpdpvvelfstpsrkt 60
   |||
OY 61 RHFNDINPVNMEFEFILDPNQENVLEITLMDANYVDETLGTATFTVSSMKVGEKKEV 120
   |||
Db 61 rhfndinpvnmefefilidpqnenvleiltmdanyvdelgtatftvssmkvgekkev 120
   |||
OY 121 PRFNOVTEVLEMSLEVSCPDLPFSMALCDQEKTFROQREHIRESKKLLGPKNSEG 180
   |||
Db 121 prfnovtevmlemslevscpdlprfsmalcdqektfrqrekhiresmkkllgpknsesg 180
   |||
OY 181 LHSARDVPVVALISGGGFRAMVFGSVKAKALYESGIIDCATYVAGLSGSTMVSTLYSH 240
   |||
Db 181 lhsardvpvvalisgggframvfgsvkalkayesgidcatyvgslsgstvmstlysh 240
   |||
OY 241 PDPEKGPPEINEELMKVNSHNPILLLPQVKRYVESLMKKSSGQPTFTDIFGMLIG 300
   |||
Db 241 pdfpekgppeeineelmknvshnpilllpqkvryveslwmkksqgptftdifgmlig 300
   |||
OY 301 ETLIHNRMNTTSLSEKYNVTAQCPLPFTCLHVRKDVSELMFADWVESPYEIGMAKYG 360
   |||
Db 301 etlinhnmnttsslsekynvtacplpftclhvrkdvselmfadwvespyeigmakyg 360
   |||
OY 361 TFMAPDLFGSKFFMGTVVKKYEENPLHFLMGVGSASFILFNRVLGVSQSRSRGTMEEE 420
   |||
Db 361 tfmapdlfgskffmgtvvkkyeenplhflmgvgsasfllfnrvlgvsgsrgstmeee 420
   |||
OY 421 LENTTKTHIVNSDSDSDSHPKGTENEDAGSDYQSDNQASWIRMTALVSDSALFN 480
   |||
Db 421 lenttkthivnsdssdsdshpkgtenedagsdyqsdngswlrmalvdsalfn 480
   |||
OY 481 TREGRAGKVNHPGLGNTSTYPLSPFATQDSFDDELDAAVADPDEFERITPELV 540
   |||
Db 481 tregragkvnhpglgnstypplsfpfatqdsfddeldaavdpdeferityepldv 540
   |||
OY 541 KSKKIHVDSGLTFNLPYLILRPGVGLITSEFSARPSDSSPPFEKELLAEKAKANN 600
   |||
Db 541 kskkihvdsgltnfnylilrpogvdlitsefsarpsdssppfekellaekakann 600
   |||
OY 601 KLPFPRIDYVFDREGLEKCYVFKPKNPMDKDCPTIIHFVLANINFRKYKAPGVPRETE 660
   |||
Db 601 klpfpridyvfdreglekcyvfkpknpmdkdcptiihfvlaninfrkykapgvyrete 660
   |||
OY 661 EKEKLENDPFIQDPPESESTFNQVQNAFKRLHDMHNTLNINIDVTEAMVESIEYKR 720
   |||
Db 661 eekelendpfiqdppeestfnqvnafkrlhdmhntlninidvteamvesieykr 720
   |||
OY 721 ONPSRCSVLSNVEARFKNKEPLSKPKA 749
   |||
Db 721 onpsrcsvlsnvearffnkeplskpka 749

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RESULT 7
AARS4090
ID AARS4090 standard: Protein: 749 AA.
XX
AC AARS4090;

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XX 01-FEB-1995 (first entry)
DT PLA2 phospholipase.
XX
XX Phospholipase: inflammatory response: prostaglandin; leukotriene;
DE testing: detection; arachidonic acid; phospholipids; PLA2.
XX
XX Homo sapiens.
OS
XX US5322776-A.
XX 21-JUN-1994.
XX
XX 28-FEB-1990; 90US-0486628.
XX
XX 28-FEB-1990; 90US-0486628.
XX
XX 13-JAN-1993; 93US-0004156.
XX
XX (GENY ) GENETICS INST INC.
XX
XX Clark J, Knopf JL;
XX
XX WPT: 1994-199533/24.
XX
XX N-PSDB; AA064162.
XX
XX DNA sequences encoding human and murine phospholipase A2 enzyme -
PT useful for detecting antiinflammatory potential of chemical
PT agents.
XX
XX Claim 1: Columns 5-10; 13pp: English.
XX
XX Prostaglandins and leukotrienes are important mediators of
XX inflammation. They are unstable and are not stored in cells but are
XX synthesised from arachidonic acid in response to stimuli.
XX Arachidonic acid itself is not free in cells but is released from
XX the sn-2 position of membrane phospholipids by phospholipase A2
XX (PLA2). Purified PLA2 can be used in methods for detecting the
XX anti-inflammatory potential of various chemical agents.
XX
SQ Sequence 749 AA:

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Query Match 99.8%; Score 3935; DB 15; Length 749;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 748; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MSFIDPYOHIIYEHQSHKFTYVVLARATVTKGAFGMDLPDPYVELFISTPDSSRKT 60
   |||
Db 1 msfidpyghllvehyshkftvvlratkvkgaigdmldpdpvvelfstpsrkt 60
   |||
OY 61 RHFNDINPVNMEFEFILDPNQENVLEITLMDANYVDETLGTATFTVSSMKVGEKKEV 120
   |||
Db 61 rhfndinpvnmefefilidpqnenvleiltmdanyvmkelgtatftvssmkvgekkev 120
   |||
OY 121 PRFNOVTEVLEMSLEVSCPDLPFSMALCDQEKTFROQREHIRESKKLLGPKNSEG 180
   |||
Db 121 prfnovtevmlemslevscpdlprfsmalcdqektfrqrekhiresmkkllgpknsesg 180
   |||
OY 181 LHSARDVPVVALISGGGFRAMVFGSVKAKALYESGIIDCATYVAGLSGSTMVSTLYSH 240
   |||
Db 181 lhsardvpvvalisgggframvfgsvkalkayesgidcatyvgslsgstvmstlysh 240
   |||
OY 241 PDPEKGPPEINEELMKVNSHNPILLLPQVKRYVESLMKKSSGQPTFTDIFGMLIG 300
   |||
Db 241 pdfpekgppeeineelmknvshnpilllpqkvryveslwmkksqgptftdifgmlig 300
   |||
OY 301 ETLIHNRMNTTSLSEKYNVTAQCPLPFTCLHVRKDVSELMFADWVESPYEIGMAKYG 360
   |||
Db 301 etlinhnmnttsslsekynvtacplpftclhvrkdvselmfadwvespyeigmakyg 360
   |||
OY 361 TFMAPDLFGSKFFMGTVVKKYEENPLHFLMGVGSASFILFNRVLGVSQSRSRGTMEEE 420
   |||

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PA (ELIL) LILLY & CO ELI.
 XX Sharp JD, Striffler BA, Cholu XC, Kramer RM, Pickard RT;
 PI
 DR WPI: 2000-181816/16.
 XX N-PSDB: AA288756, AA288757.
 XX
 PT An isolated amino acid having phospholipase (PLA2) activity is useful
 PT in assays to identify inhibitors having a therapeutic benefit, such as
 PT inhibiting the central role of PLA2 in the inflammatory component of
 PT Alzheimer's disease -
 PS Claim 1: Column 53-58; 32pp; English.
 CC This invention describes a novel human phospholipase A2 (PLA2) protein
 CC (I) and its encoding nucleic acid. The amino acid (I) releases
 CC arachidonic acid in specific tissues characterized by unique membrane
 CC phospholipids, by generating lysophospholipid species which are
 CC deleterious to membrane integrity or by remodeling of unsaturated species
 CC of membrane phospholipids through deacylation/reacylation mechanisms. The
 CC amino acid is useful in assays to identify inhibitors having a
 CC therapeutic benefit, such as inhibiting the central role of PLA2 in the
 CC inflammatory component of Alzheimer's disease. The amino acid (I) allows
 CC sensitive and rapid screening and identification of inhibitors of
 CC phospholipase A2. This sequence represents the human PLA2 protein (also
 CC known as phosphatide 2-acyl hydrolase).
 XX
 XX Sequence 913 AA:
 SQ
 Query Match 18.4%; Score 724; DB 21; Length 913;
 Best Local Similarity 24.8%; Pred. NO. 1.3e-58;
 Matches 208; Conservative 152; Mismatches 268; Indels 210; Gaps 26;
 QY 21 TVVVRATVVTGAGGMDTDPVVELEFISTPDSRKTRFNFNDINVMETPEFLID 80
 DB 145 TVRVIGHNIPSS--Kdlvtpsdcytlwlpacshrltvtvkssssvwmgsfflrh 201
 QY 81 PNOENVLETTLDANVM-DELTGATFVSSMKVGE-----KKEYPF--- 122
 DB 202 rqlkhvmeklvtdgdlvtgddpvlsvlfdagtlrgefresfsispqgegilevfrfq 261
 QY 123 -----TENOV-----TEKVL----- 132
 DB 262 sladrgewlvsngvlvarelsclhvgleedgdkasehrvqlvvpsscqpgeaavgtgt 321
 QY 133 -----FMSLEVCSCP----- 143
 DB 322 ftfhpcwcegeislrlqdaeeq[kap]salpsggvtrlvfrtqgeplmrvclkkeag] 381
 QY 144 ----LRFSMALDOEKTFRQQRKEHRESMKRLGPKNSEGLHSARDVPVAALILSGSGGF 199
 DB 382 relavrlgfgpaeeqafslrrkqvaaalrqel---qldgdlqedealpvalmatg991 438
 QY 200 RAVGFSGVKMLYSGILDCATYVAGLSGSTWYMSLTYSHPDFPEK---GPEEINEELM 256
 DB 439 ramtelvlgqlaglkelyldlcvsyiltgaagstawaanlyedpewqkdlagptel---lk 495
 QY 257 KVVNSHPFLLLLPQVKRYVESIMKKSSGQVPTFDIGMILIGELLINRMT--TISL 315
 DB 496 tcytknklyvlpesqldqyrgqlaeearllypsctfnlwa--lineallndeprdhklsq 554
 QY 316 KERVNTAQCPLPLFTCLHYK-PDVSELMFADWVEFSPYEIGNAKYGTFWAPDLFGSKFPM 374
 DB 555 relahngqrp[ly]alcnlckgslttfegwceitsp[ly]vpgkylafpsliffsefm 614
 QY 375 GTVVVKYEENPLPHFTMGWGSAPSLIFNRVLCVSGSQSGSTMEEL-----ENITTH 428
 DB 615 gqimkrllp[est]icfl[eg]l[ys]n[yl]a-----anldqsl[yl]asepsqfwdrw 658
 QY 428 IYSNDSDDSD-----ESHHPKGTENEDAGSDYQSDNQASWIRIMTALVSDALFNTTRG 484
 DB 659 vrnngnldkeqypllkleepstacgrla--effld-----llwtrp 697

QY 485 RAGVHNFMGLGINTSYPLSP[SD]FA[QD]SEFDD[EL]AAVADPDEFRIYEPLDVNSK 544
 DB 698 laqathnflrjghfhkdyfqp[hp]-hftwkattldgl-----pqg-----llpseph 742
 QY 545 IHVVDGSLTENLPPYLIRPQGVLLIISFDSFARSOSSPPEFKLLLAEKAKNNKLPE 604
 DB 743 lcldvgyllnscipllqprtdvdlisldynlga-----fqqllqllgrfcqegipf 797
 QY 605 PKIDYVDRBGLKCYEYFK-PKNPDMKDCPTIHFPLANINPKRYKAPGVPRTEDEK 663
 DB 798 plpspspeeqqlprechtlsp[ct]p-----gapavlhrlvsostlreysapgy-rltpeea 852
 QY 664 ETADFDIEDPESPSTENFQYRNOAFKRLHDMHFNFLNNDIVKEAMVESIEYRQ 721
 DB 853 aagevnl-ssdsqpyhckvysqgedvckllhltlyvncmneqlllealrqavrrrq 909
 RESULT 10
 ID AAB74635 standard; Protein; 913 AA.
 XX AAB74635;
 AC AAB74635;
 XX 23-MAY-2001 (first entry)
 DT
 XX
 DE Phospholipase A2 (PLA2) protein sequence SEQ ID NO:3.
 XX
 KM Phospholipase A2; PLA2; antiinflammatory; inflammatory condition;
 KM Rheumatoid arthritis; psoriasis; asthma; cytosolic PLA2; cPLA2.
 OS Homo sapiens.
 PN US6197569-B1.
 PD 06-MAR-2001.
 XX
 PF 07-FEB-2000; 2000US-0500358.
 XX
 PR 29-MAR-1996; 96US-0014608.
 PR 19-MAR-1997; 97US-0041264.
 PR 28-MAR-1997; 97US-0827208.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX Cholu XC, Kramer RM, Pickard RT, Sharp JD, Striffler BA;
 PI
 DR WPI: 2001-256372/26.
 XX N-PSDB: AAF74998, AAF74999.
 PT Novel nucleic acid molecules encoding phospholipase A2 enzyme, useful
 PT in screening assays for identifying compounds that inhibit or block
 PT phospholipase A2 enzyme activity -
 PS Claim 1: Column 53-58; 32pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I),
 CC comprising a 3085 base pair phospholipase A2 (PLA2) sequence (given in
 CC AAF74999), encoding a 913 residue phospholipase A2 protein sequence
 CC (given in AAB74635), or a nucleotide sequence which hybridizes under
 CC stringent conditions to the above mentioned nucleotide sequence. Also
 CC described are: (1) an isolated polynucleotide (II) comprising an 8517
 CC base pair sequence, given in AAF74998; (2) an expression vector (III)
 CC comprising (I) and an expression control sequence; (3) a host cell
 CC transformed with (III); (4) an expression vector (IV) comprising (II)
 CC operably linked to an expression control sequence; and (5) a host cell
 CC transformed with (IV). (I) is useful for screening compounds which
 CC inhibit or block cytosolic PLA2 (cPLA2) enzyme activity. The host cells
 CC transformed or transfected with cPLA2 enzymes in large
 CC quantities which are useful in screening assays for discovering agents
 CC that inhibit PLA2. The inhibitors identified are useful for treating
 CC inflammatory conditions such as rheumatoid arthritis, psoriasis, or
 CC asthma. (I) is also useful in the detection of mutant genomic DNA which

[illegible]

Query Match	15.7%	Score 619	DB 21	Length 605
Best Local Similarity	27.1%	Pred. No. 4.6e-49		
Matches 174	Conservative 125	Mismatches 238	Indels 106	Gaps 22
100	ENLGNATFTVSSMKYGEKKEVPEFINOVYEMVLEMS-----LEVSCDPLRFSMALCDOE	154		
44	eslsvagagvqvrdlgsldpprlgfrtscslpsawdyrlrela-----vrigfpcpcae	99		
155	KTFROORKEHIRESMKLLGPKNSBGLHSARDPVVAITGSGGFRAMVFGCVKALYE	214		
100	qafllrrkqvnaalrtgal---qlgdglqdeqlpvalmataggytramtsllysglaqlke	156		
215	SGIIDCATYVAGLSGSTWYMSLYLSHPPERK---GREINIELMKNVSHNPLLLTPQK	271		
157	lglllcvsylylbaasgswalaanlyadpewsqdlagrtel---lktqvknklyvdlapsq	213		
272	VKRYVESLMMKKSSQAPYTFDTDFMCLGELTILHNRMMNT--TSSLKKEKNYTAQCPRLPT	330		
214	lqrryqelaerarrlylpsocflnwa--lneallheophdhktsdgrealsghnqrpplyc	272		
331	CLHVR- PDVSELMFADWVEFSPEYETIGMAKYGTFMADLFSGSFENGTVYKKKEENPLFL	389		
273	antngsgsltfefgewecfspyevgfrkygaflpselgfsefmgqlmkrlpselcfl	332		
390	MGVMSAASFILERNVLGVSGSQSRGSTMEEL-----ENITTKHIVNSDSSDD----	439		
333	eglwshnlyr-----anldslsyawespsqfwdtivrngandlkeqyrl	376		
440	ESHEBKGTENEDAGSDYOSDNOQASWIHRMIMALVDSALFNTREGRACKVHNFMGLNEN	499		
377	kleepstagraia--efftd-----lltwrplaqgthnflgylhfh	415		
500	TSYPLSLSDPRTQOSFDDDELDAAVADPDEFERIRTEPLDVASKKIHVWDSLTNTLPRP	559		
416	kdyfghp--hstkwatctldgl-----pnq-----ltpsephclldvylintscrl	460		
560	LILRQNGVDLITISDFESAPSDSPPEFKELLAEKMAKMNKLPPKPIDYUVDREGLKE	619		
461	pllgtrtdvdlisldynlha-----fgdqljllrfcogegiprbrlpspspeeqdlpre	515		
620	CYVER- PKNPMEKDCPTLIHFVLANINFRKAYKAGVPRTEEEKELADFDIDPDESPE	678		
516	chtfddpccp---gapavlnhf-----ssgv-rtfpeaaagavnl-sssdpy	558		

OY 679 STNFOIPNOAFKRLDLMHFTLNNDIVIKEMVESIEYRRQ 721
 Db 559 hycKvYsgedvdklhlthynvcnqegllleaIrgvqrrr 601

RESULT 13

AAW75132
 ID AAW75132 standard; Protein; 483 AA.

AC AAW75132;

XX 28-JAN-1999 (first entry)

DE Human secreted protein encoded by gene 11 clone HCNJ40.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

OS Homo sapiens.

XX Homo sapiens.

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WC0839446-A2.

11-SEP-1998.

06-MAR-1998; 98MO-US04492.

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07-MAR-1997; 97US-0040162.

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07-MAR-1997; 97US-0040626.

07-MAR-1997; 97US-0043312.

07-MAR-1997; 97US-0043312.

07-MAR-1997; 97US-0043313.

07-MAR-1997; 97US-0043314.

07-MAR-1997; 97US-0043315.

07-MAR-1997; 97US-0043568.

07-MAR-1997; 97US-0043569.

07-MAR-1997; 97US-0043576.

07-MAR-1997; 97US-0043576.

07-MAR-1997; 97US-0043580.

07-MAR-1997; 97US-0043669.

WC0839446-A2.

11-SEP-1998.

06-MAR-1998; 98MO-US04492.

07-MAR-1997; 97US-0038621.

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07-MAR-1997; 97US-0043313.

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07-MAR-1997; 97US-0040334.

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07-MAR-1997; 97US-0043568.

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07-MAR-1997; 97US-0043669.

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07-MAR-1997; 97US-0043569.

07-MAR-1997; 97US-0043576.

XX	Claim 1; page 326-327; 447pp; English
PS	

CC This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line.
CC The gene can be used to generate fusion proteins by linking to the gene
CC to a human immunoglobulin Fc portion (e.g. AAV34145) for increasing the
CC stability of the fused protein as compared to the human protein only.
CC The invention relates to 70 novel genes and their fragments (nucleic
CC acid sequences: AAV34154-V34276; amino acid sequences AAW5057-W5179)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 70
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34154 for described uses).

SQ Sequence 483 AA;

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Best Local Similarity	28.8%;	Pred. No. 3.1e-48;		

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Db	61	el---lkqvcknk1gvlapagqlqdrvgelaeraar1gypseftnlwa-1lneal1hdeph	116	
QY	310	T-TLSSLKEKVNATQCPRLPFLTCLAHK-PRVSELMFADWVEFYEYEGMAKGTGFMAPDL	367	
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QY	368	FGSKFEFMGTVVKKYEENPLHFMGVGSAFSLFNRYLGVSGSGSRGSTMEEEL-----	421	
Db	177	fgseftmgqlmkrlr1pearic1c1eg1kwnal9a-----an1qds1ywasep	220	
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Db	221	sqfwdvrwngqan1dkeqvr1lklleppstagra--e1ftd-----	260	
QY	478	LENTEGRAGKGVHNPMGLNLTGYRPLSPLSDFATQPSFDDELDAVADDERERYER	537	
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QY	538	LDRVSKK1HHVVDSCGLTFNMLPRLLIRPQKQGLTFSFDSARPSDSSPPEKELLAEKWA	597	
Db	305	1tpeaphc1ld1vgyl1ntsc1rlp1lqprtcd1l1s1d1yn1hga-----1gq1d1l1gr1fc	359	
QY	598	KMKK1LRPKIDPYVFDREGLKECYEVR-PKKNPMKEKDCPTI1NFVLIN1NFRKYKARGVP	656	
Db	360	qegq1r1fp1r1ps1p1s1p1eeq1q1p1rc1t1fs1d1p1t1c1p1-----1gav1l1h1r1l1vs1ds1f1r1e1ys1ap1v	414	
QY	657	RETEKERK1AOFD1FDDPESPEFSFNQYRQAKRKL1DL1HNF1L1N1D1V1K1EAMWESI	716	
Db	415	rttpeaaagevnl-ssadedp1y1ktvtyaqedvdk1l1h1l1h1vncvnaqel1lea1rtgav	473	
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Db	474	qr1r1q 478		
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ID	AAW75067 standard; Protein: 483 AA.			
XX	AAW75067:			
XX	28-JAN-1999 (first entry)			

RESULT	14
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ID	AAW75067 standard; Protein; 483 AA
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AC	AAW75067;
XX	
DT	28-JAN-1999 (first entry)

XX Human secreted protein encoded by gene 11 clone HCEHJ40.
DE

KM Human secreted protein; fusion protein; gene therapy; protein therapy;
 KM diagnosis; cancer; tumour; neurodegenerative disorder; leukaemia;
 KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KM developmental abnormality; foetal deficiency; blood; allergy; renal;
 KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KM inflammatory; ischemic shock; Alzheimer's disease; osteoarthritis; AIDS;
 KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm;

05 Homo sapiens

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FT /label= unknown

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PN W09839446-A2

PD 11-SEP-1998.

PF 06-MAR-1998; 98WO-US04492

PR	07-MAR-1997	97US-0038651
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PR	23-MAY-1997	97US-0047600

PR	23-MAY-1997;	97US-0047601.
PR	23-MAY-1997;	97US-0047612.
PR	23-MAY-1997;	97US-0047613.
PR	23-MAY-1997;	97US-0047614.
PR	23-MAY-1997;	97US-0047615.
PR	23-MAY-1997;	97US-0047617.
PR	23-MAY-1997;	97US-0047618.
PR	23-MAY-1997;	97US-0047632.
PR	23-MAY-1997;	97US-0047633.
PR	06-JUN-1997;	97US-0048964.
PR	22-AUG-1997;	97US-0056630.
PR	22-AUG-1997;	97US-0056631.
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PR	22-AUG-1997;	97US-0056637.
PR	22-AUG-1997;	97US-0056662.
PR	22-AUG-1997;	97US-0056664.
PR	22-AUG-1997;	97US-0056845.
PR	22-AUG-1997;	97US-0056862.
PR	22-AUG-1997;	97US-0056864.
PR	22-AUG-1997;	97US-0056872.
PR	22-AUG-1997;	97US-0056874.
PR	22-AUG-1997;	97US-0056875.
PR	22-AUG-1997;	97US-0056876.
PR	22-AUG-1997;	97US-0056877.
PR	22-AUG-1997;	97US-0056878.
PR	22-AUG-1997;	97US-0056879.
PR	22-AUG-1997;	97US-0056880.
PR	22-AUG-1997;	97US-0056881.
PR	22-AUG-1997;	97US-0056882.
PR	22-AUG-1997;	97US-0056893.
PR	22-AUG-1997;	97US-0056894.
PR	22-AUG-1997;	97US-0056903.
PR	22-AUG-1997;	97US-0056908.
PR	22-AUG-1997;	97US-0056909.
PR	22-AUG-1997;	97US-0056910.
PR	22-AUG-1997;	97US-0056911.
PR	05-SEP-1997;	97US-0057650.
PR	05-SEP-1997;	97US-0057651.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Bednarik DP, Brewer LA, Carter KC, Duan R, Edner R, Endress GA;	
PI	Feng P, Ferrite AM, Fischer CL, Graves KA, Greene JM, Hu JS;	
PI	Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;	
PI	Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;	
XX		
XX	WPI: 1998-609887/51.	
DR	N-PSDB: AAV34164.	
XX		
PT	New isolated human genes and the secreted polypeptides they encode	
PT	- useful for diagnosis and treatment of e.g. cancers, neurological	
PT	disorders, immune diseases, inflammation or blood disorders	
XX		
XX	Claim 1; Page 285-287; 447p; English.	
XX		
CC	This sequence represents a secreted human protein encoded by the gene	
CC	clone detailed in the descriptor line.	
CC	The gene can be used to generate fusion proteins by linking to the gene	
CC	to a human immunoglobulin Fc portion (e.g. AAV34165) for increasing the	
CC	stability of the fused protein as compared to the human protein only.	
CC	The invention relates to 70 novel genes and their fragments (nucleic	
CC	acid sequences: AAV34164-34276; amino acid sequences AAV75057-W75179)	
CC	which are useful for preventing, treating or ameliorating medical	
CC	conditions e.g. by protein or gene therapy. Also, pathological	
CC	conditions can be diagnosed by determining the amount of the new	

CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 70
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34154 for described uses).

SQ **Sequence** **483 AA;**

Query Match	15.4%	Score 608.5;	DB 19;	Length 483;
Best Local Similarity	28.8%	Pred. No. 3.1e-48;		
Matches 157; Conservative	107;	Mismatches	198;	Indels 83; Gaps 18

QY 193 LGS6GGFRAMVGFSGVMKALYESGILDCATYVAGLSGSTWYMSTLYSHDPPEK---GPE 2499

db 1 matggyiramtstlygqlaqlkelgllcdasyiltgasgstwalanlykdpewsqkdlagpt 60

[illegible]

310 T-TISSLKEKVNMAOCPIPIETCTIHYK-BDVSEIMFADWVFSPVETGMARVGTETMAPDI 367

Db 117 dhklsdgreals hqnp lpi ycalntkxqslttfegewcefs pyevgf pkygafip sel 176

QY 368 FGSKFMGTIVKRYEENPLHFLMGVWGSASFILFNRLGVSGSGRGSTMEEL----- 421

Db 177 fgseffmgqlmkrlpsericflegiwsnlya-----anlgdslywasep 220

422 ENIIHIVSNBSSBDD---ESHEPKLENDAGSDIQSDNQASMIHRMIALVSUSA 4//

00 478 1ENMDECBAGVHNEM/CI NI NTSVYR SDI SDEATONSDNDEI DAUAVDDBDEFFRIVED 5337

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Db      261  -lltwrlaqatnflrqlhfhkdyfghp--hfstwkattldg]-----pnq----- 304

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QY 538 LDVSKSIHVVDSGLTENLPYPLILRPQGVDTISFDF SARPSDSSPFEKELLAEKWA 5977

Db 305 ltpsephicildvy1intscip1qgrtrvd11sldynlnga-----fgq1q1grfc 359

Q7 398 KNNKLPFKPIDPVEFDREGLEKCYVFK-PANPDMERKDCPTLIHFVLANINFRKKYKAGVP 656

[illegible]

Db 415 rtbeaaagevn]-ssdsphvktvtsqedvdkllhthvncnqee]lealrgav 473

QY 717 EYRQ 721

Db 474 qrrrq 478

RESULT 15

AM020571
ID AAB28997 standard; Protein; 541 AA.

AC AAB28997;
XY

DT 01-FEB-2001 (first entry)
XX

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XX
XX

of course prochlorazone regime.

XXXXXXX

KM EST.
XX

05 Homo sapiens.
XX

XX 10-SEP-2000

XX 09-JUL-1997; 97US-0890615.
PF

